

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:32:55 ; Search time 30 Seconds
(without alignments)
1196.041 Million cell updates/sec

Title: US-10-820-714A-1-HIS15

Perfect score: 2251

Sequence: 1 NDVARGIVKADVAQHSYGLY.....EVQAYNVPVGPQTFSIAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2242	99.6	434	2 US-09-985-689A-1	Sequence 1, Appli
2	2242	99.6	640	2 US-09-509-814A-6	Sequence 6, Appli
3	2242	99.6	640	2 US-09-920-954-6	Sequence 6, Appli
4	2237	99.4	640	2 US-09-509-814A-8	Sequence 8, Appli
5	2237	99.4	640	2 US-09-920-954-8	Sequence 8, Appli
6	2186	97.1	434	2 US-09-985-689A-2	Sequence 2, Appli
7	2178	96.8	639	2 US-09-509-814A-4	Sequence 4, Appli
8	2178	96.8	639	2 US-09-920-954-4	Sequence 4, Appli
9	2150	95.5	639	2 US-09-509-814A-1	Sequence 1, Appli
10	2150	95.5	639	2 US-09-920-954-1	Sequence 1, Appli
11	2150	95.5	640	2 US-09-509-814A-2	Sequence 2, Appli
12	2150	95.5	640	2 US-09-920-954-2	Sequence 2, Appli
13	2138	95.0	434	2 US-09-985-689A-6	Sequence 6, Appli
14	2125.5	94.4	433	2 US-09-985-689A-7	Sequence 7, Appli
15	2125.5	94.4	641	1 US-08-873-479-42	Sequence 42, Appli
16	1998.5	88.8	433	2 US-09-985-689A-5	Sequence 5, Appli
17	1994.5	88.6	433	2 US-09-985-689A-3	Sequence 3, Appli
18	1987.5	88.3	433	2 US-09-985-689A-4	Sequence 4, Appli
19	1986.5	88.2	433	2 US-09-104-623A-4	Sequence 4, Appli
20	1986.5	88.2	433	2 US-09-019-532-4	Sequence 4, Appli
21	1986.5	88.2	433	2 US-09-338-746-4	Sequence 4, Appli
22	1986.5	88.2	635	1 US-08-873-479-43	Sequence 43, Appli
23	1581.5	70.3	345	2 US-09-512-251A-10	Sequence 10, Appli
24	1581.5	70.3	345	2 US-09-515-150A-10	Sequence 10, Appli
25	1581.5	70.3	345	2 US-09-196-281-13	Sequence 13, Appli
26	1581.5	70.3	345	2 US-10-336-324-10	Sequence 10, Appli
27	452.5	20.1	659	2 US-08-894-818B-1	Sequence 1, Appli

28	452.5	20.1	659	2 US-09-445-472-12	Sequence 12, Appli
29	452.5	20.1	659	2 US-10-090-624-12	Sequence 12, Appli
30	452.5	20.1	659	2 US-09-841-553-1	Sequence 1, Appli
31	414	18.4	412	2 US-09-445-472-1	Sequence 1, Appli
32	414	18.4	412	2 US-10-090-624-1	Sequence 1, Appli
33	414	18.4	522	2 US-08-894-818B-3	Sequence 3, Appli
34	414	18.4	522	2 US-09-445-472-4	Sequence 4, Appli
35	414	18.4	522	2 US-10-090-624-4	Sequence 4, Appli
36	414	18.4	522	2 US-09-841-553-3	Sequence 3, Appli
37	414	18.4	654	2 US-08-894-818B-35	Sequence 35, Appli
38	414	18.4	654	2 US-09-445-472-16	Sequence 16, Appli
39	414	18.4	654	2 US-10-090-624-16	Sequence 16, Appli
40	414	18.4	654	2 US-09-841-553-35	Sequence 35, Appli
41	401	17.8	659	2 US-08-894-818B-5	Sequence 5, Appli
42	401	17.8	659	2 US-09-841-553-5	Sequence 5, Appli
43	343.5	15.3	734	2 US-09-000-016-4	Sequence 4, Appli
44	343.5	15.3	734	2 US-09-514-340-4	Sequence 4, Appli
45	343.5	15.3	823	2 US-09-000-016-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-985-689A-1
; Sequence 1, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1

Query Match	99.6%	Score 2242;	DB 2;	Length 434;
Best Local Similarity	99.8%	Pred. No. 4.1e-174;		
Matches 433;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	NDVARGIVKADVAQHSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN	60	
Db	1	NDVARGIVKADVAQHSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN	60	
QY	61	NANDTNGHGHVAGSVLGNSTNKGMAQANLVFOSIMDSGGGLGSLPSNLQTLFSQAYS	120	
Db	61	NANDTNGHGHVAGSVLGNSTNKGMAQANLVFOSIMDSGGGLGSLPSNLQTLFSQAYS	120	
QY	121	AGARLHTNSWGAANVAGYTTDSRNVDYVKNDMTILFAAGNEGPNGGTISAPGTAKNAI	180	
Db	121	AGARLHTNSWGAANVAGYTTDSRNVDYVKNDMTILFAAGNEGPNGGTISAPGTAKNAI	180	
QY	181	TVGATENLRPSFGSYADNINHVQFSRGPTKDGRIKPDVMAPGTIFLSARSLAPDSF	240	
Db	181	TVGATENLRPSFGSYADNINHVQFSRGPTKDGRIKPDVMAPGTIFLSARSLAPDSF	240	
QY	241	WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKGRTIPKPSLLKAAIAGAADIGLY	300	

Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNGGWRVTLDKSLNVAYNNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 420
Db 361 SVTLVNDLVLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434
RESULT 2
US-09-509-814A-6
; Sequence 6, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR FILING DATE: 1998-10-07
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-6

Query Match 99.6%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 7.le-174;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAOHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAOHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSGVSADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSLAPDSF 240
Db 387 TVGATENLRPSGVSADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSLAPDSF 446
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 506
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNGGWRVTLDKSLNVAYNNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 566

QY 361 SVTLVNDLVLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 420
Db 567 SVTLVNDLVLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 3
US-09-920-954-6
; Sequence 6, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JF98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-6

Query Match 99.6%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 7.le-174;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAOHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAOHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSGVSADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSLAPDSF 240
Db 387 TVGATENLRPSGVSADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSLAPDSF 446
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 506
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Db 507 PNGNGGWRVTLDKSLNVAYNNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 420
Db 567 SVTLVNDLVLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434

Db 627 VPVGPQTFSLAIVN 640
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RESULT 4

US-09-509-814A-8

; Sequence 8, Application US/09509814A

; Patent No. 6376227

; GENERAL INFORMATION:

; APPLICANT: TAKAIWA, MIKIO

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUYOSHI

; APPLICANT: KUBOTA, HIROMI

; APPLICANT: HITOMI, JUN

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SHIKATA, SHITSUM

; APPLICANT: NOMURA, MASAFUMI

; TITLE OF INVENTION: ALKALINE PROTEASE

; FILE REFERENCE: 0327-0832-OPCT

; CURRENT APPLICATION NUMBER: US/09/509,814A

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: PCT/JP98/04528

; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 640

; TYPE: PRT

; ORGANISM: Bacillus sp.

US-09-509-814A-8

Query Match 99.4%; Score 2237; DB 2; Length 640;

Best Local Similarity 99.5%; Pred. No. 1.8e-173;

Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
|||||
Db 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
|||||
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
|||||
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326
|||||
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180
|||||
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 386
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QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
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Db 387 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 446
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QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIIGLY 300
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Db 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIIGLY 506
|||||
QY 301 PNGQGWGRVTLDKSLNAVYVNESSLSTSQATYSFTATAGKPLKISLVMSDAPASTTA 360
|||||
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSTSQATYSFTATAGKPLKISLVMSDAPASTTA 566
|||||
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWGRNNVNFVINAPOSQGTITIEVQAYN 420
|||||
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWGRNNVNFVINAPOSQGTITIEVQAYN 626
|||||
QY 421 VPVGPQTFSLAIVN 434
|||||
Db 627 VPVGPQTFSLAIVN 640
|||||

RESULT 6

US-09-985-689A-2

; Sequence 2, Application US/09985689A

; Patent No. 6803222

; GENERAL INFORMATION:

; APPLICANT: HATADA, YUJI

; APPLICANT: OGAWA, AKINORI

; APPLICANT: KAGEYAMA, YASUSHI

```
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-2

Query Match          97.1%; Score 2186; DB 2; Length 434;
Best Local Similarity 96.3%; Pred. No. 1.5e-169;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVQAHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVQAHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGAYTTDSRNVDVYRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANGAYTTDSRNVDVYRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADVGLGY 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADVGLGY 300
QY 301 PNGNCGWRVTLDKSLNVAQYVNGDFTSPYNDNWDGRNNVNFVINAPOSQGTYYIEVQAYN 420
Db 301 PNGNCGWRVTLDKSLNVAQYVNGDFTSPYNDNWDGRNNVNFVINAPOSQGTYYIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 7
US-09-509-814A-4
; Sequence 4, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; FILE REFERENCE: 0327-0832-OPCT
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; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-4

Query Match          96.8%; Score 2178; DB 2; Length 639;
Best Local Similarity 96.1%; Pred. No. 1.1e-168;
Matches 417; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVQAHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 206 NDVARGIVKADVQAHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLQTLFSQAYS 120
Db 266 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARIHTNSWGAANGAYTTDSRNVDVYRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 326 AGARIHTNSWGAANGAYTTDSRNVDVYRKNDMTILFAAGNERPNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSF 240
Db 386 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSF 445
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADVGLGY 300
Db 446 WANHDSKYAYMGTSMTATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADVGLGY 505
QY 301 PNGNCGWRVTLDKSLNVAQYVNGDFTSPYNDNWDGRNNVNFVINAPOSQGTYYIEVQAYN 420
Db 506 PNGNCGWRVTLDKSLNVAQYVNGDFTSPYNDNWDGRNNVNFVINAPOSQGTYYIEVQAYN 565
QY 361 SVTLVNDLVLITAPNGTQYVNGDFTSPYNDNWDGRNNVNFVINAPOSQGTYYIEVQAYN 420
Db 566 SVTLVNDLVLITAPNGTQYVNGDFTSPYNDNWDGRNNVNFVINAPOSQGTYYIEVQAYN 625
QY 421 VPVGPQTFSLAIVN 434
Db 626 VPVGPQTFSLAIVN 639

RESULT 8
US-09-920-954-4
; Sequence 4, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
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; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 639
; TYPE: PRP
; ORGANISM: Bacillus sp.
US-09-920-954-4

Query Match          96.8%; Score 2178; DB 2; Length 639;
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QY 421 VPGVGPOTPSLAIVN 434
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; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 639
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; ORGANISM: Bacillus sp.
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OTHER INFORMATION: Xaa is any amino acid

US-09-509-814A-1

Query Match 95.5%; Score 2150; DB 2; Length 639;
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Matches 417; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 206 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 266 NANDTNGHGHVAGSVLGNSTKGMAPQANLVFQSIMDSXGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMILFAAGNEGNGGTISAPGTAKNAI 180
DB 326 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMILFAAGNEGNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240

DB 386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 445
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLCY 300
DB 446 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLCY 505
QY 301 PNGNQWGRVTLDKSLNVAIYVNESSLSTSKATYSFTATAGKPKIKISLVMSDAPASTTA 360
DB 506 PNGNQWGRVTLDKSLNVAIYVNESSLSTSKATYSFTATAGKPKIKISLVMSDAPASTTA 565
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWDRNVENVFINAPOSGTYTIEVQAYN 420
DB 566 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWDRNVENVFINAPOSGTYTIEVQAYN 625
QY 421 VPVGPQTFSLAIVN 434
DB 626 VPVGPQTFSLAIVN 639
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; Sequence 1, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: PRT
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US-09-920-954-1

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Best Local Similarity 96.1%; Pred. No. 2,1e-166;
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DB 206 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
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DB 326 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILSARSSLAPDSSF 240
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; Sequence 2, Application US/09509814A
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; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUMI
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
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US-09-509-814A-2

Query Match      95.5%; Score 2150; DB 2; Length 640;
Best Local Similarity 96.1%; Pred. No. 2.1e-166;
Matches 417; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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DB 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTCGRNDSMHEAPRGKITALYALGRTN 266

QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSXGGLGGLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSWGAANGVAYTTDSNRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSWGAANGVAYTTDSNRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

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DB 387 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGCTFILSARSLAPDSSF 446

QY 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGLY 300
DB 447 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGLY 506

QY 301 PNGNQGWGRVTLDKSLNVAIVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAIVNESSLSSTSQATYFTATAGKPLKISLVWSDAPASTTA 566

QY 361 SVTLVNDLVLVTPAGNGTOYVGNDFTPSYNDNWDGRNVENVPINAPQSGTYYTIEVQAYN 420
DB 567 SVTLVNDLVLVTPAGNGTYVGNDFXXPPXXNWDGRNVENVPINXQSGTYYTIEVQAYN 626

QY 421 VPGVGPOTFSLAVN 434
DB 627 VPGVGPOTFSLAVN 640

RESULT 12
US-09-920-954-2
; Sequence 2, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 640
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; TYPE: PRT
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: Xaa is any amino acid
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; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
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; OTHER INFORMATION: Xaa is any amino acid
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; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (149)..(149)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (161)..(161)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (166)..(166)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (173)..(173)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
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LOCATION: (188)..(188)
NAME/KEY: misc feature
LOCATION: (189)..(189)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
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LOCATION: (287)..(287)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (307)..(307)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (325)..(325)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (370)..(370)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (432)..(432)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (502)..(502)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (532)..(532)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (542)..(542)
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NAME/KEY: misc feature
LOCATION: (596)..(596)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (597)..(597)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (612)..(612)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (633)..(633)
OTHER INFORMATION: Xaa is any amino acid

Query Match 95.5%; Score 2150; DB 2; Length 640;
Best Local Similarity 96.1%; Pred. No. 2.1e-166;
Matches 417; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVQAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITAIYALGRN 60
DB 207 NDVARGIVKADVQAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITAIYALGRN 266
QY 61 NANDTNGHGTAVAGSVLNGSTNKGMAQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGTAVAGSVLNGSTNKGMAQANLVFQSIIMDSXGGLGGLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 446
QY 241 WANHDSKVAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGAADIGLY 300
DB 447 WANHDSKVAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGAADIGLY 506
QY 301 PNGNQWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNQWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNVENVFINAPOSGTTTIEVQAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNVENVFINAPOSGTTTIEVQAYN 626
QY 421 VPVGPQTFSLAVN 434
DB 627 VPVGPQTFSLAVN 640
RESULT 13
US-09-985-689A-6
Sequence 6, Application US/09985689A
Patent No. 6803222
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: OGAWA, AKINORI
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAKI, KATSUHIISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in version 3.1
SEQ ID NO 6
LENGTH: 434
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-985-689A-6

Query Match 95.0%; Score 2138; DB 2; Length 434;
Best Local Similarity 93.3%; Pred. No. 1.2e-165;
Matches 405; Conservative 19; Mismatches 10; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVQAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITAIYALGRN 60
DB 1 NDVARGIVKADVQAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITAIYALGRN 60
QY 61 NANDTNGHGTAVAGSVLNGSTNKGMAQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTAVAGSVLNGSTNKGMAQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMAVLFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGLGY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGLGY 300
QY 301 PNGNQGWGRVTLDKSLNVAVNETSSLSTSQKATYSFTATAGKPLKISLWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAVNETSSLSTSQKATYSFTATAGKPLKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTTYIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTKYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTTYIEVOAYN 420
QY 421 VPVGPOTFSLAIYN 434
DB 421 VPQGPQAFSLAIYN 434

RESULT 14
US-09-985-689A-7
; Sequence 7, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHII
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHII
; APPLICANT: SAEKI, KATSUHISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-7

Query Match 94.4%; Score 2125.5; DB 2; Length 433;
Best Local Similarity 93.5%; Pred. No. 1.2e-164;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQNFGYLGQGIIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDPNGHGHVAGSVLGN-ATNKGMAQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
QY 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 120 AGARHTNSWGAAPVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 179
QY 181 TVGATENLRPSFGSVADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSSF 240
DB 180 TVGATENLRPSFGSVADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSSF 239
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGLGY 300
DB 240 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADVGLGF 299
QY 301 PNGNQGWGRVTLDKSLNVAVNETSSLSTSQKATYSFTATAGKPLKISLWSDAPASTTA 360

DB 300 PNGNQGWGRVTLDKSLNVAVNETSSLSTSQKATYSFTATAGKPLKISLWSDAPGSTTA 359
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTTYIEVOAYN 420
DB 360 SVTLVNDLVLITAPNGTKYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTTYIEVOAYN 419
QY 421 VPVGPOTFSLAIYN 434
DB 420 VPVGPOTFSLAIHV 433

RESULT 15
US-08-873-479-42
; Sequence 42, Application US/08873479
; Patent No. 5891701
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan
; APPLICANT: Lynne, Christianson
; TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
; TITLE OF INVENTION: Having Protease Activity
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSES: No. 5891701o No. 5891701disk of No. 5891701th America
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,479
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Agis, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 5251.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-873-479-42

Query Match 94.4%; Score 2125.5; DB 1; Length 641;
Best Local Similarity 93.5%; Pred. No. 2.1e-164;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTN 60
DB 209 NDVARGIVKADVAQNFGYLGQGIIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTN 268
QY 61 NANDTNGHGHVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 269 NANDPNGHGHVAGSVLGN-ATNKGMAQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 327
QY 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 328 AGARHTNSWGAAPVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 387
QY 181 TVGATENLRPSFGSVADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSSF 240

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Db	448	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF	507
Qy	301	PNGNQGWGRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVMSDAPASTTA	360
Db	508	PNGNQGWGRVTLDKSLNVAFNETSPLSTSQKATYSFTAQAGKPLKISLVMSDAPGSTTA	567
Qy	361	SVTLVNDLDLVITAPNGTQYVGNDFTSFYNDNWDGRNNVNFINAPQSGTYTIEVQAYN	420
Db	568	SVTLVNDLDLVITAPNGTKYVGNDFTPYDNNWDGRNNVNFINAPQSGTYTIEVQAYN	627
Qy	421	VPVGPQTFSLAIVN	434
Db	628	VPVSPQTFSLAIVH	641

Search completed: April 7, 2006, 09:33:33
Job time : 31 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:36:15 ; Search time 91 Seconds
(without alignments)
2095.499 Million cell updates/sec

Title: US-10-820-714A-1
Perfect score: 2247
Sequence: 1 NDVARGIVKADVAQSSYGILY.....EQVAYNPVGPQTFSLAIVN 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2247	100.0	434	5	AAm50080	AAm50080 Bacillus
2	2247	100.0	434	7	ADY33778	Ady33778 Bacillus
3	2247	100.0	434	7	ADZ51757	Adz51757 Wild-type
4	2247	100.0	434	8	ADL25802	Adl25802 Bacillus
5	2247	100.0	434	8	ADM40771	Adm40771 Mature al
6	2247	100.0	434	8	ADSI4427	Adsi4427 Bacillus
7	2247	100.0	434	8	ADT49604	Adt49604 Bacillus
8	2247	100.0	640	2	AAV17090	AAv17090 Bacillus
9	2247	100.0	640	8	ADM40773	Adm40773 Alkaline
10	2247	100.0	640	8	ADS14437	Adsi14437 Bacillus
11	2247	100.0	641	8	ADT49613	Adt49613 Bacillus
12	2242	99.8	434	8	ADM40780	Adm40780 Alkaline
13	2242	99.8	434	8	ADS14441	Adsi14441 Bacillus
14	2242	99.8	640	2	AAV17091	AAv17091 Bacillus
15	2239	99.6	434	8	ADS14438	Adsi14438 Bacillus
16	2239	99.6	434	8	ADS14442	Adsi14442 Bacillus
17	2238	99.6	434	8	ADS14439	Adsi14439 Bacillus
18	2232	99.3	434	8	ADS14440	Adsi14440 Bacillus
19	2230	99.2	434	8	ADS14443	Adsi14443 Bacillus
20	2225	99.0	434	8	ADS14444	Adsi14444 Bacillus
21	2210	98.4	434	8	ADS14445	Adsi14445 Alkaline
22	2215	97.7	436	8	ADM40787	Adm40787 Bacillus
23	2191	97.5	434	5	AAm50081	AAm50081 Bacillus
24	2191	97.5	434	7	ADZ51758	Adz51758 Mutant Ba

25	2191	97.5	434	8	ADM40779	Adm40779 Alkaline
26	2183	97.2	639	2	AAV17089	AAv17089 Bacillus
27	2155	95.9	639	2	AAV17087	AAv17087 An alkali
28	2155	95.9	640	2	AAV17088	AAv17088 An alkali
29	2143	95.4	434	5	AAm50085	AAm50085 Bacillus
30	2143	95.4	434	7	ADZ51762	Adz51762 Mutant Ba
31	2143	95.4	434	8	ADM40784	Adm40784 Alkaline
32	2130.5	94.8	433	8	ADS52078	Adsi52078 Bacillus
33	2130.5	94.8	433	8	ADS52011	Adsi52011 Bacillus
34	2129.5	94.8	433	8	ADS52082	Adsi52082 Bacillus
35	2126.5	94.6	433	8	ADS52083	Adsi52083 Bacillus
36	2125.5	94.6	433	5	AAm50086	AAm50086 Bacillus
37	2125.5	94.6	433	7	ADZ51763	Adz51763 Mutant Ba
38	2125.5	94.6	433	8	ADM40785	Adm40785 Alkaline
39	2125.5	94.6	433	8	ADS52010	Adsi52010 Bacillus
40	2125.5	94.6	433	8	ADS52016	Adsi52016 Bacillus
41	2125.5	94.6	433	8	ADS52001	Adsi52001 Bacillus
42	2125.5	94.6	641	2	AAW89547	AAw89547 Bacillus
43	2123.5	94.5	433	8	ADS52062	Adsi52062 Bacillus
44	2123.5	94.5	433	8	ADS52054	Adsi52054 Bacillus
45	2122.5	94.5	433	8	ADS52087	Adsi52087 Bacillus

ALIGNMENTS

RESULT 1
AAm50080
ID AAm50080 standard; protein; 434 AA.
XX
AC AAm50080;
XX
DT 12-AUG-2002 (first entry)
XX
DE Bacillus sp KSM-KP43 alkaline protease protein fragment.
XX
KW Alkaline protease; detergent; laundry; bleaching; dishwasher.
XX
OS Bacillus sp.
XX
PN EP1209233-A2.
XX
PD 29-MAY-2002.
XX
PF 22-NOV-2001; 2001EP-00127851.
XX
PR 22-NOV-2000; 2000JP-00355166.
PR 12-APR-2001; 2001JP-00114048.
XX
PA (KAOS) KAO CORP.
XX
PI Hatada Y, Ogawa A, Kageyama Y, Sato T, Araki H, Sumitomo N;
PI Okuda M, Saeki K;
XX
DR WPI; 2002-437518/47.
XX
PT New modified alkaline proteases useful in detergent compositions.
PS Claim 1; Page 10-11; 25pp; English.
CC This invention describes novel Bacillus sp. alkaline proteases useful in
CC detergent compositions, especially in laundry, bleaching or automatic
CC dishwasher detergents. The novel proteases have an increased detergency *
CC (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This
CC sequence represents a fragment of the alkaline protease KP43 from
CC Bacillus sp strain KSM-KP43 which is used to create the modified protease
CC represented in AAm50090
SQ Sequence 434 AA;

Query Match 100.0%; Score 2247; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159; Indels 0; Gaps 0;
Matches 434; Conservative 0; Mismatches 0;

PS		Claim 1; SEQ ID NO 1; 31pp; English.
XX		The invention relates to an alkaline protease having a fully defined
CC		sequence of 434 amino acids (I) given in the specification, or an amino
CC		acid sequence at least 80% homology with (I), where an amino acid residue
CC		at position 65, 101, 163, 170, 171, 273, 320, 359 or 387 of (I) is
CC		selected from 16 amino acid residues. The amino acid residues at the
CC		corresponding positions are selected from: position 65: proline; position
CC		101: asparagine; position 163: histidine, aspartic acid, phenylalanine,
CC		lysine, asparagine, serine, isoleucine, leucine, glutamine, threonine or
CC		valine; position 170: valine or leucine; position 171: alanine, glutamic
CC		acid, glycine or threonine; position 273: isoleucine, glycine or
CC		threonine; position 320: phenylalanine, valine, threonine, leucine,
CC		isoleucine or glycine; position 359: serine, leucine, valine, isoleucine
CC		or glutamic acid; and position 387: alanine, lysine, glutamine, glutamic
CC		acid, arginine or histidine. The alkaline protease is useful for the
CC		production of a detergent composition, such as laundry detergent, fiber
CC		modifiers, leather-treating agents, cosmetic compositions, bath
CC		additives, food modifiers and pharmaceutical compositions. The alkaline
CC		protease may also be used as bleaching detergent, hard surface cleaning
CC		detergent, pipe cleaner, artificial tooth cleaner, and as a sterilizing
CC		cleanser for medical tools. The new alkaline protease has a more potent
CC		proteolytic capacity, exhibiting excellent detergency for the removal of
CC		a complex stain, and has high secretion capacity. This sequence
CC		corresponds to the Bacillus sp. alkaline protease.
XX		
SQ	Sequence 434 AA;	
Query Match		100.0%; Score 2247; DB 7; Length 434;
Best Local Similarity		100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	NDVARGIVKADVAAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRGKITALYALGRTN 60
Db	1	NDVARGIVKADVAAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRGKITALYALGRTN 60
QY	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY	121	AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db	121	AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKGRIPKPDVMAPTFILSARSSLAPDSSF 240
Db	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKGRIPKPDVMAPTFILSARSSLAPDSSF 240
QY	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
Db	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
QY	301	PNGNQGWGRVTLDKSLNVAYVNESLSTSQKATYSFTATAGPKPLKISLVWSDAPASTTA 360
Db	301	PNGNQGWGRVTLDKSLNVAYVNESLSTSQKATYSFTATAGPKPLKISLVWSDAPASTTA 360
QY	361	SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDGGRNNVENVFINAPQSGTYTIEVQAYN 420
Db	361	SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDGGRNNVENVFINAPQSGTYTIEVQAYN 420
QY	421	VPVGPQTFSLAIVN 434
Db	421	VPVGPQTFSLAIVN 434
RESULT 3		
ADZ51757		ADZ51757 standard; protein; 434 AA.
XX	XX	ADZ51757;
XX	XX	ADZ51757;
DT	DT	16-JUN-2005 (first entry)
XX	XX	

QY	1	NDVARGIVKADVAAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRGKITALYALGRTN 60
Db	1	NDVARGIVKADVAAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRGKITALYALGRTN 60
QY	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY	121	AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db	121	AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKGRIPKPDVMAPTFILSARSSLAPDSSF 240
Db	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKGRIPKPDVMAPTFILSARSSLAPDSSF 240
QY	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
Db	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
QY	301	PNGNQGWGRVTLDKSLNVAYVNESLSTSQKATYSFTATAGPKPLKISLVWSDAPASTTA 360
Db	301	PNGNQGWGRVTLDKSLNVAYVNESLSTSQKATYSFTATAGPKPLKISLVWSDAPASTTA 360
QY	361	SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDGGRNNVENVFINAPQSGTYTIEVQAYN 420
Db	361	SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDGGRNNVENVFINAPQSGTYTIEVQAYN 420
QY	421	VPVGPQTFSLAIVN 434
Db	421	VPVGPQTFSLAIVN 434
RESULT 2		
ADZ33778		
ID	ID	ADY33778 standard; protein; 434 AA.
XX	XX	ADY33778;
AC	AC	ADY33778;
DT	DT	05-MAY-2005 (first entry)
XX	XX	Bacillus species alkaline protease.
DE	DE	Bacillus species alkaline protease.
XX	XX	mutagenesis; alkaline protease; detergent; laundry; cosmetic; food;
KW	KW	bleaching detergent.
XX	XX	
OS	OS	Bacillus sp.
XX	XX	EP1347044-A2.
PN	PN	
PD	PD	24-SEP-2003.
XX	XX	
PF	PF	21-MAR-2003; 2003EP-00006472.
XX	XX	
PR	PR	22-MAR-2002; 2002JP-00081428.
PR	PR	06-JUN-2002; 2002JP-00165987.
PR	PR	18-OCT-2002; 2002JP-00304230.
PR	PR	18-OCT-2002; 2002JP-00304231.
XX	XX	
PA	PA	(KAOS) KAO CORP.
XX	XX	
PI	PI	Okuda M, Sato T, Saito K, Sumitomo N, Izawa Y, Saeki K;
PI	PI	Kobayashi T, Nomura M;
XX	XX	
DR	DR	WPI; 2003-846540/79.
DR	DR	N-PSDB; ADY33779.
XX	XX	
PT	PT	New alkaline protease having specific amino acid residue at a specific
PT	PT	position of its amino acid sequence, useful for producing detergent
PT	PT	compositions, laundry detergent, fiber modifiers, leather-treating agents
PT	PT	or pipe cleaners.
XX	XX	

DE Wild-type Bacillus sp. alkali protease.
XX alkali protease; enzyme; surfactant; mutagenesis.
KW Bacillus sp.
XX JP2003125783-A.
XX 07-MAY-2003.
XX 26-OCT-2001; 2001JP-00329472.
XX 26-OCT-2001; 2001JP-00329472.
XX (KAOS) KAO CORP.
XX WPI; 2003-856569/80.
XX New alkali protease useful for preparing detergents comprises
PT substitution mutations at 251 or 256 position of protease KP43 derived
PT from Bacillus species KSM-KP43.
XX
PS Claim 1; SEQ ID NO 1; 16pp; Japanese.
XX The invention relates to a mutant alkali protease having an amino acid
CC deletion at position(s) 251 or 256 in a fully defined sequence given as
CC SEQ ID No:1 in the specification, or the following amino acid residue
CC Asp, Gly, Ala, Asp, Thr, Ile, Val, Leu or Glu at position 251, or the
CC amino acid residue Lys, Ser Phe, Arg, Tyr, Met, Thr, Ile, Val, Leu, or
CC Glu at position 256. Also described are: (i) an alkali protease having
CC the amino acid sequence of SEQ ID No:1, or having 60% or more homology to
CC SEQ ID No:1, or a deletion of amino acid corresponding to position 251 or
CC 256, (ii) a gene which encodes an alkali protease, (iii) a recombinant
CC vector containing the gene, and (iv) a transformed organism containing
CC the recombinant vector. The alkali protease sequence having 60% or more
CC homology to SEQ ID No:1 is chosen from a fully defined sequence selected
CC from SEQ ID Nos 2-7 as given in the specification. The transformed
CC organism is a microorganism. The mutant alkali protease is useful for
CC preparing detergents. The mutant alkali protease exhibits high resistance
CC against oxidizing agent. The mutant alkali protease has high specific
CC activity. This sequence represents wild-type Bacillus sp. alkali
XX protease.
SQ Sequence 434 AA;
Query Match 100.0%; Score 2247; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAOSSGLYGGQGIIVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAOSSGLYGGQGIIVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTGVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSVADNINHAQFSSRGPTKDGRIKPDVMAQPGTIFILSARSSSLAPDSSF 240
DB 181 TVGATENLRPSFGSVADNINHAQFSSRGPTKDGRIKPDVMAQPGTIFILSARSSSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITTPKPSLLKAALIAGAADIGLGY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITTPKPSLLKAALIAGAADIGLGY 300
QY 301 PNGQGWGRVTLDKSLNVAAYVNESSLSSTSKATYSFTATAGKPKIKISLVMSDAPASTTA 360
DB 301 PNGQGWGRVTLDKSLNVAAYVNESSLSSTSKATYSFTATAGKPKIKISLVMSDAPASTTA 360

QY 361 SVTLVNDLVLITAPNGTOYVGNDFTSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTOYVGNDFTSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420
QY 421 VPVGQPTFSLAIVN 434
DB 421 VPVGQPTFSLAIVN 434
RESULT 4
ADL25802
ID ADL25802 standard; protein; 434 AA.
XX
AC ADL25802;
XX
DT 20-MAY-2004 (first entry)
XX
DE Bacillus alkaline protease.
XX
KW alkaline protease; washing agent; enzyme.
XX
OS Bacillus sp.
XX
PN JP2004008085-A.
XX
PD 15-JAN-2004.
XX
PF 06-JUN-2002; 2002JP-00165950.
XX
PR 06-JUN-2002; 2002JP-00165950.
XX
PA (KAOS) KAO CORP.
XX
DR WPI; 2004-094297/10.
DR N-PSDB; ADL25803.
XX
PT Novel mutant alkaline protease produced by substituting the amino acid
PT residues useful as washing agent.
XX
PS Claim 1; SEQ ID NO 1; 21pp; Japanese.
XX
CC The invention comprises a mutant Bacillus alkaline protease which
CC contains substitutions at positions 163, 170 and 434. The mutant alkaline
CC protease is useful as a washing agent. The present amino acid sequence
CC represents a Bacillus alkaline protease of the invention.
XX
SQ Sequence 434 AA;
Query Match 100.0%; Score 2247; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAOSSGLYGGQGIIVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAOSSGLYGGQGIIVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTGVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSVADNINHAQFSSRGPTKDGRIKPDVMAQPGTIFILSARSSSLAPDSSF 240
DB 181 TVGATENLRPSFGSVADNINHAQFSSRGPTKDGRIKPDVMAQPGTIFILSARSSSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITTPKPSLLKAALIAGAADIGLGY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITTPKPSLLKAALIAGAADIGLGY 300
QY 301 PNGQGWGRVTLDKSLNVAAYVNESSLSSTSKATYSFTATAGKPKIKISLVMSDAPASTTA 360

Db 301 PGNQGWGRVTLDSKLNVAIVYNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
QY 361 SVTLVNDLDLVIITAPNGTQVVGNDFTSPYNDNDGRNNVENVFINAPQSGTYTIEVQAYN 420
Db 361 SVTLVNDLDLVIITAPNGTQVVGNDFTSPYNDNDGRNNVENVFINAPQSGTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 5
ADM40771
ID ADM40771 standard; protein; 434 AA.
XX
AC ADM40771;
XX
DT 01-JUL-2004 (first entry)
XX
DE Mature alkaline protease from Bacillus sp. KSM-KP43.
XX
KW alkaline protease; laundry detergent; bleaching agent; detergent;
KW denture-cleaning agent; enzyme.
XX
OS Bacillus sp.; KSM-KP43.
XX
XX US2004072321-A1.
PN
XX
PD 15-APR-2004.
XX
XX 09-JUN-2003; 2003US-00456479.
PF
XX
XX 26-JUN-2002; 2002JP-00186387.
PR
PR 18-OCT-2002; 2002JP-00304232.
XX
XX (KAOS) KAO CORP.
PA
PI Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
XX
XX WPI: 2004-328572/30.
DR N-PSDB; ADM40772.

XX New alkaline protease having a mutant prepro sequence where amino acid
PT residues at positions 52, 75 and 142 are substituted with another amino
PT acid residue, useful as enzyme component of laundry detergents, or
PT bleaching agents.
XX
PS Claim 1; SEQ ID NO 2; 29pp; English.

XX The invention relates to an alkaline protease having a prepro sequence.
XX The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
CC acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
CC acid residues at: (a) position 52 is substituted by aspartic acid or
CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
CC position 142 is substituted by lysine. The alkaline protease is useful as
CC an enzyme which can be incorporated into laundry detergents, bleaching
CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
CC cleaning agents, and detergents for sterilising medical apparatus. The
CC present sequence represents mature alkaline protease from Bacillus sp.
CC KSM-KP43.
XX
SQ Sequence 434 AA;

Query Match 100.0%; Score 2247; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNGKMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

Db 61 NANDTNGHGHVAGSVLNGSTNGKMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNCGPNGGTTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNCGPNGGTTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINNHVAQFSSRGPTKDGRIKPDVMAFGTFLISARSSILAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINNHVAQFSSRGPTKDGRIKPDVMAFGTFLISARSSILAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNGITTPKPSLLKAALAGAADIGILGY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNGITTPKPSLLKAALAGAADIGILGY 300
QY 301 PGNQGWGRVTLDSKLNVAIVYNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PGNQGWGRVTLDSKLNVAIVYNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
QY 361 SVTLVNDLDLVIITAPNGTQVVGNDFTSPYNDNDGRNNVENVFINAPQSGTYTIEVQAYN 420
Db 361 SVTLVNDLDLVIITAPNGTQVVGNDFTSPYNDNDGRNNVENVFINAPQSGTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 6
ADS14427
ID ADS14427 standard; protein; 434 AA.
XX
AC ADS14427;
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43 mature protein SEQ ID NO:1.
XX
KW protease; enzyme; alkaline protease; laundry detergent; KP43.
XX
OS Bacillus sp.; KSM-KP43.
XX
PN EP1466962-A1.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008604.
XX
XX 10-APR-2003; 2003JP-00106709.
PR (KAOS) KAO CORP.
XX
XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
PI WPI: 2004-711313/70.
XX N-PSDB; ADS14428.
DR
XX New engineered alkaline protease, useful particularly in laundry
PT detergents, comprising specified amino acids at particular positions.
XX
XX Claim 1; SEQ ID NO 1; 31pp; English.

XX The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents the wild-type Bacillus sp. KSM-KP43 alkaline

```
CC protease, KP43.
XX
SQ Sequence 434 AA;

Query Match      100.0%; Score 2247; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSVGLYGQGOIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSVGLYGQGOIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALTAGAADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALTAGAADIGLY 300
Qy 301 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Qy 361 SVTLVNDLDLIVITAPNGTOYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLDLIVITAPNGTOYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Qy 421 VPVGQPTFSLAIYN 434
Db 421 VPVGQPTFSLAIYN 434

RESULT 7
ADT49604
ID ADT49604 standard; protein; 434 AA.
AC ADT49604;
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease mature protein fragment.
XX
KW Alkaline protease; detergent; fiber modification; leather processing;
KW cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
XX
OS Bacillus sp. KSM-KP43.
XX
PN EF1466970-A1.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008605.
XX
PR 10-APR-2003; 2003JP-00106708.
XX
PA (KAOS ) KAO CORP.
XX
PI Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
XX
DR WPI; 2004-711317/70.
DR N-PSDB; ADT49605.
XX
PT New engineered alkaline protease with improved activity and thermal
stability, useful particularly in detergents such as laundry detergents.

Claim 1; SEQ ID NO 1; 35pp; English.

The invention relates to an alkaline protease and its encoding gene. The
alkaline protease can be expressed by standard recombinant methodology.
The alkaline protease is useful in the industry particularly in
detergents such as laundry detergents, but also in fiber modifying
agents, leather processing agents, cosmetic compositions, bath additives,
food-modifying agents, and pharmaceuticals. The enzyme has good activity
and thermal stability. The present sequence represents a mature alkaline
protease from Bacillus sp. KSM-KP43.

Sequence 434 AA;

Query Match      100.0%; Score 2247; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSVGLYGQGOIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSVGLYGQGOIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALTAGAADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALTAGAADIGLY 300
Qy 301 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Qy 361 SVTLVNDLDLIVITAPNGTOYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLDLIVITAPNGTOYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Qy 421 VPVGQPTFSLAIYN 434
Db 421 VPVGQPTFSLAIYN 434

RESULT 8
AAV17090
ID AAV17090 standard; protein; 640 AA.
XX
AC AAV17090;
XX
DT 20-MAR-2003 (revised)
DT 21-JUL-1999 (first entry)
XX
DE Bacillus alkaline protease.
XX
KW Alkaline protease; Bacillus; casein digestion; oleic acid; enzyme;
KW washing composition; oxidising agent.
XX
OS Bacillus sp.
XX
PN WO9918218-A1.
XX
PD 15-APR-1999.
XX
PF 07-OCT-1998; 98WO-JP004528.
XX
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```
PR 07-OCT-1997; 97JP-00274570.
XX (KAOS ) KAO CORP.
XX
XX Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;
XX Shikata S, Nomura M;
XX WPI; 1999-287736/27.
DR N-PSDB; AAX37278.
XX
XX Alkali protease from Bacillus used in washing powders.
PT
XX
XX Disclosure; Page 58-63; 71pp; Japanese.
XX
XX The invention relates to alkaline proteases produced by strains of
CC Bacillus. The proteases ability to digest casein is not inhibited by
CC oleic acid and they have a high stability to oxidising agents. The
CC alkaline protease of the invention has the following properties: (a) it
CC is active over the pH range 4-13 and has at least 80% of its optimum
CC activity over the range pH 6-12; (b) after 30 minutes at 40 deg. C it is
CC stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)
CC its ability to digest casein is not inhibited by oleic acid; (e) it has
CC molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can
CC used as enzymes in washing compositions for use in automatic dishwashers
CC and for washing clothes. The stability to oxidising agents allows the
CC enzyme to be an effective component of washing compositions including
CC bleaches. The present sequence represents an alkaline protease. (Updated
CC on 20-MAR-2003 to correct DR field.)
XX
XX Sequence 640 AA;
XX
Query Match 100.0%; Score 2247; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.1e-158;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHEAPRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHEAPRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKPDVMAFGTILSARSSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKPDVMAFGTILSARSSLAPDSSF 446
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAAALIAGAADIGLGY 300
DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAAALIAGAADIGLGY 506
QY 301 PNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKATYFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKATYFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLDDIVITAPNGTQVGNDFTPYNDNDGRNVENFINAPQSGTYTIEVQAYN 420
DB 567 SVTLVNDLDDIVITAPNGTQVGNDFTPYNDNDGRNVENFINAPQSGTYTIEVQAYN 626
QY 421 VPVGPOTFSLAIYN 434
DB 627 VPVGPOTFSLAIYN 640
RESULT 9
ADMA40773
ID ADM40773 standard; protein; 640 AA.
XX
XX AC ADM40773;
```

```
XX DT 01-JUL-2004 (first entry)
XX DE Alkaline protease from Bacillus sp. KSM-KP43.
XX KW alkaline protease; laundry detergent; bleaching agent; detergent;
XX denture-cleaning agent; enzyme.
XX OS Bacillus sp.; KSM-KP43.
XX PN US2004072321-A1.
XX PD 15-APR-2004.
XX PF 09-JUN-2003; 2003US-00456479.
XX PR 26-JUN-2002; 2002JP-00186387.
XX PR 18-OCT-2002; 2002JP-00304232.
XX PA (KAOS ) KAO CORP.
XX PI Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
XX WPI; 2004-328572/30.
XX DR N-PSDB; ADM40772.
XX PT New alkaline protease having a mutant prepro sequence where amino acid
PT residues at positions 52, 75 and 142 are substituted with another amino
PT acid residue, usefull as enzyme component of laundry detergents, or
PT bleaching agents.
XX PS Disclosure; SEQ ID NO 4; 29pp; English.
XX CC The invention relates to an alkaline protease having a prepro sequence.
CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
CC acid residues having 80% homology or higher to SEQ ID NO: 1, where amino
CC acid residues at: (a) position 52 is substituted by aspartic acid or
CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
CC position 142 is substituted by lysine. The alkaline protease is usefull as
CC an enzyme which can be incorporated into laundry detergents, bleaching
CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
CC cleaning agents, and detergents for sterilising medical apparatus. The
CC present sequence represents alkaline protease from Bacillus sp. KSM-KP43.
XX SQ Sequence 640 AA;
XX
Query Match 100.0%; Score 2247; DB 8; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.1e-158;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHEAPRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHEAPRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKPDVMAFGTILSARSSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKPDVMAFGTILSARSSLAPDSSF 446
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAAALIAGAADIGLGY 300
DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAAALIAGAADIGLGY 506
QY 301 PNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKATYFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKATYFTATAGKPLKISLVWSDAPASTTA 566
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QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 626
QY 421 VPVGPQTFSLAIVN 434
DB 627 VPVGPQTFSLAIVN 640

RESULT 10
ADS14437
ID ADS14437 standard; protein; 640 AA.
XX
AC ADS14437;
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43.
XX
KW protease; enzyme; alkaline protease; laundry detergent; KP43.
XX
OS Bacillus sp.; KSM-KP43.
XX
FH Key Location/Qualifiers
FT Peptide 1..206
FT Protein 207..640
XX
PN EP1466962-A1.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008604.
XX
PR 10-APR-2003; 2003JP-00106709.
XX
PA (KAOS) KAO CORP.
XX
PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
DR WPI; 2004-711313/70.
DR N-PSDB; ADS14428.
XX
PT New engineered alkaline protease, useful particularly in laundry
FT detergents, comprising specified amino acids at particular positions.
XX
PS Disclosure; SEQ ID NO 1; 31pp; English.
XX
CC The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents the wild-type Bacillus sp. KSM-KP43 alkaline
CC protease, KP43. The sequence is shown in the sequence listing as part of
CC SEQ ID NO:1
XX
SQ Sequence 640 AA;

Query Match 100.0%; Score 2247; DB 8; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.1e-158;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGLPSNLQTLFSQAYS 120

DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPCTAKNAI 180
DB 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPCTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKPDVMAFGTFTLSARSSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKPDVMAFGTFTLSARSSLAPDSSF 446
QY 241 WANHDSKYAYMGTSNATPIVAGNVAQLRHFVKNRGITPKPSLLKAALTAGADIIGY 300
DB 447 WANHDSKYAYMGTSNATPIVAGNVAQLRHFVKNRGITPKPSLLKAALTAGADIIGY 506
QY 301 PNGNQGWRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB 507 PNGNQGWRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLVMSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 626
QY 421 VPVGPQTFSLAIVN 434
DB 627 VPVGPQTFSLAIVN 640

RESULT 11
ADT49613
ID ADT49613 standard; protein; 641 AA.
XX
AC ADT49613;
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease.
XX
KW Alkaline protease; detergent; fiber modification; leather processing;
KW cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
XX
OS Bacillus sp. KSM-KP43.
XX
FH Key Location/Qualifiers
FT Peptide 1..206
FT Protein 207..641
FT /note= "specifically claimed mature protein (SEQ ID 1)"
XX
PN EP1466970-A1.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008605.
XX
PR 10-APR-2003; 2003JP-00106708.
XX
PA (KAOS) KAO CORP.
XX
PI Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
DR WPI; 2004-711317/70.
DR N-PSDB; ADT49605.
XX
PT New engineered alkaline protease with improved activity and thermal
PT stability, useful particularly in detergents such as laundry detergents.
XX
PS Disclosure; Page 19-25; 35pp; English.
XX
CC The invention relates to an alkaline protease and its encoding gene. The
CC alkaline protease can be expressed by standard recombinant methodology.
CC The alkaline protease is useful in the industry particularly in
CC detergents such as laundry detergents, but also in fiber modifying

CC agents, leather processing agents, cosmetic compositions, bath additives,
CC food-modifying agents, and pharmaceuticals. The enzyme has good activity
CC and thermal stability. The present sequence represents an alkaline
CC protease from *Bacillus* sp. KSM-KP43.

XX Sequence 641 AA;

Query Match 100.0%; Score 2247; DB 8; Length 641;
Best Local Similarity 100.0%; Pred. No. 1.1e-158;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIKADVQAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIKADVQAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLGNSTNGKMAQANLVFQSIMDSGGGLGSLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLGNSTNGKMAQANLVFQSIMDSGGGLGSLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLPSPSGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF 240
DB 387 TVGATENLPSPSGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF 446
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 506
QY 301 PNGNQGWGRVTLDKSLNVAIVNNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAIVNNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQVGNDFTPSYNDWNWGRNNVENFINAPQSGTYTIEVQAYN 420
DB 567 SVTLVNDLVLITAPNGTQVGNDFTPSYNDWNWGRNNVENFINAPQSGTYTIEVQAYN 626
QY 421 VPVGPOTFSLAIYN 434
DB 627 VPVGPOTFSLAIYN 640

RESULT 12
ADM40780
ID ADM40780 standard; protein; 434 AA.

XX AC ADM40780;

XX 01-JUL-2004 (first entry)

DE Alkaline protease #2 from *Bacillus* sp. KSM-KP9865.

XX alkaline protease; laundry detergent; bleaching agent; detergent;
XX denture-cleaning agent; enzyme.

XX *Bacillus* sp.; KSM-KP9865.

XX US2004072321-A1.

XX 15-APR-2004.

XX 09-JUN-2003; 2003US-00456479.

XX 26-JUN-2002; 2002JP-00186387.

XX 18-OCT-2002; 2002JP-00304232.

XX (KAOS) KAO CORP.

XX Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;

XX WPI; 2004-328572/30.

XX
PT
PT
PT
XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

New alkaline protease having a mutant prepro sequence where amino acid
residues at positions 52, 75 and 142 are substituted with another amino
acid residue, useful as enzyme component of laundry detergents, or
bleaching agents.

Disclosure; SEQ ID NO 11; 29pp; English.

The invention relates to an alkaline protease having a prepro sequence.
The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
acid residues at: (a) position 52 is substituted by aspartic acid or
arginine; (b) position 75 is substituted by alanine or arginine; and (c)
position 142 is substituted by lysine. The alkaline protease is useful as
an enzyme which can be incorporated into laundry detergents, bleaching
agents, detergents for cleaning hard surfaces or drainpipes, denture-
cleaning agents, and detergents for sterilising medical apparatus. The
present sequence represents an alkaline protease used in homology
comparison with alkaline protease from *Bacillus* sp. KSM-KP43.

XX Sequence 434 AA;

Query Match 99.8%; Score 2242; DB 8; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-158;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIKADVQAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIKADVQAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTNGKMAQANLVFQSIMDSGGGLGSLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLGNSTNGKMAQANLVFQSIMDSGGGLGSLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLPSPSGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF 240
DB 181 TVGATENLPSPSGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
QY 301 PNGNQGWGRVTLDKSLNVAIVNNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAIVNNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQVGNDFTPSYNDWNWGRNNVENFINAPQSGTYTIEVQAYN 420
DB 361 SVTLVNDLVLITAPNGTQVGNDFTPSYNDWNWGRNNVENFINAPQSGTYTIEVQAYN 420
QY 421 VPVGPOTFSLAIYN 434
DB 421 VPVGPOTFSLAIYN 434

RESULT 13

ADS14441

ID ADS14441 standard; protein; 434 AA.

XX AC ADS14441;

XX 30-DEC-2004 (first entry)

DE *Bacillus* alkaline protease KP43 N187S mutant.

XX protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;

XX KW mutein.

XX *Bacillus* sp.; KSM-KP43.

OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 187 /note= "Wild-type Asn substituted by Ser"
FT
PN EP1466962-A1.
XX 13-OCT-2004.
XX 08-APR-2004; 2004EP-00008604.
XX 10-APR-2003; 2003JP-00106709.
XX (KAOS) KAO CORP.
XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayaashi T;
PI WPI; 2004-711313/70.
XX New engineered alkaline protease, useful particularly in laundry
PT detergents, comprising specified amino acids at particular positions.
XX
XX Example 1; Page; 31pp; English.
XX The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents an alkaline protease variant of the invention. Note:
CC The present sequence is not represented in the specification, but has
CC been created by the indexer using sequence shown in ADS14427 and
CC information given in Example 1.
XX
XX Sequence 434 AA;
SQ

Query Match 99.8%; Score 2242; DB 8; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-158;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSGIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSGIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARITHNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARITHNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNHNHVAQSSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSFF 240
DB 181 TVGATESLRPSFGSYADNHNHVAQSSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSFF 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
QY 301 PNGNGGWGRVTLDKSLNVAAYNVESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNGGWGRVTLDKSLNVAAYNVESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYYIEQAYN 420
DB 361 SVTLVNDLVLITAPNGTQVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYYIEQAYN 420

QY 421 VPVGQPTFSLAIVN 434
DB 421 VPVGQPTFSLAIVN 434

RESULT 14
AAV17091
ID AAY17091 standard; protein; 640 AA.
XX
AC AAY17091;
XX
DT 20-MAR-2003 (revised)
DT 21-JUL-1999 (first entry)
XX
DE Bacillus alkaline protease.
XX
KW Alkaline protease; Bacillus; casein digestion; oleic acid; enzyme;
KW washing composition; oxidising agent.
XX
OS Bacillus sp.
XX WO9918218-A1.
PN
XX 15-APR-1999.
PD
XX 07-OCT-1998; 98WO-JP004528.
PF
XX 07-OCT-1997; 97JP-00274570.
PR
XX (KAOS) KAO CORP.
PA
XX Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;
PI Shikata S, Nomura M;
XX
DR WPI; 1999-287736/27.
DR N-PSDB; AAX37279.
XX
PT Alkali protease from Bacillus used in washing powders.
XX
PS Disclosure; Page 63-68; 71pp; Japanese.
XX
CC The invention relates to alkaline proteases produced by strains of
CC Bacillus. The proteases ability to digest casein is not inhibited by
CC oleic acid and they have a high stability to oxidising agents. The
CC alkaline protease of the invention has the following properties: (a) it
CC is active over the pH range 4-13 and has at least 80% of its optimum
CC activity over the pH range 6-12; (b) after 30 minutes at 40 deg. C it is
CC stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)
CC its ability to digest casein is not inhibited by oleic acid; (e) it has
CC molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be
CC used as enzymes in washing compositions for use in automatic dishwashers
CC and for washing clothes. The stability to oxidising agents allows the
CC enzyme to be an effective component of washing compositions including
CC bleaches. The present sequence represents an alkaline protease. (Updated
CC on 20-MAR-2003 to correct DR field.)
XX
SQ Sequence 640 AA;
Query Match 99.8%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 2.5e-158;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 266
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSGIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSGIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARITHNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARITHNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Db 327 AGARIHTNSWGAAYNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVWAPGTFILSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVWAPGTFILSARSSLAPDSSF 446
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLGY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLGY 506
Qy 301 PNGNOGWRVTLDKSLNVAYNVNESSLSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNOGWRVTLDKSLNVAYNVNESSLSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVINAPOSQGTVTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVINAPOSQGTVTIEVOAYN 626
Qy 421 VPVGPQTFSIAIWN 434
Db 627 VPVGPQNFSLAIWN 640

RESULT 15
ADS14438
ID ADS14438 standard; protein; 434 AA.
XX
AC ADS14438;
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43 S15H/S16T mutant.
KW protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;
KW mutain.
XX
OS Bacillus sp.; KSM-KP43.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 15 /note= "Wild-type Ser substituted by His"
FT Misc-difference 16 /note= "Wild-type Ser substituted by Thr"
FT
PN EP1466962-Al.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008604.
XX
PR 10-APR-2003; 2003JP-00106709.
XX
PA (KAOS) KAO CORP.
XX
PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayaashi T;
XX
DR WPI; 2004-711313/70.
XX
FT New engineered alkaline protease, useful particularly in laundry
FT detergents, comprising specified amino acids at particular positions.
XX
XX
XX Example 1; Page: 31pp; English.

XX The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC

CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents an alkaline protease variant of the invention. Note:
CC The present sequence is not represented in the specification, but has
CC been created by the indexer using sequence shown in ADS14427 and
CC information given in Example 1.
XX

SQ Sequence 434 AA;

Query Match 99.6%; Score 2239; DB 8; Length 434;
Best Local Similarity 99.5%; Pred. No. 2.5e-158;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHTYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFOSIMDSSGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFOSIMDSSGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAYNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAYNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVWAPGTFILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVWAPGTFILSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLGY 300
Db 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLGY 300
Qy 301 PNGNOGWRVTLDKSLNVAYNVNESSLSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNOGWRVTLDKSLNVAYNVNESSLSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVINAPOSQGTVTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVINAPOSQGTVTIEVOAYN 420
Qy 421 VPVGPQTFSIAIWN 434
Db 421 VPVGPQTFSIAIWN 434

Search completed: April 7, 2006, 09:37:55
Job time : 92 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:39:04 ; Search time 40 Seconds
(without alignment)
1043.952 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNPVPGPTFSIAIYN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1.*
- 2: Pir2.*
- 3: Pir3.*
- 4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523.5	23.3	1743	2 T18279	multidrug resistan
2	497	22.1	1905	2 T18267	multidrug resistan
3	347.5	15.5	444	2 B83891	intracellular alka
4	320.5	14.3	442	2 A69587	intracellular alka
5	310.5	13.8	806	2 A41341	microbial serine p
6	302.5	13.5	1398	2 T28159	pyrolysin (EC 3.4.
7	283	12.6	580	2 S11890	serine proteinase
8	281	12.5	419	1 S25835	subtilisin (EC 3.4
9	280	12.5	799	2 G83753	subtilisin-type pr
10	279.5	12.4	1345	2 T29090	surface layer-asso
11	277	12.3	420	1 S23407	subtilisin (EC 3.4
12	267	11.9	715	2 JC4908	alkaline serine pr
13	263	11.7	1331	2 A72647	probable surface l
14	259.5	11.5	757	2 C84120	subtilisin-type pr
15	257.5	11.3	513	1 A35742	aqualysin (EC 3.4.
16	253.5	11.3	894	2 F69730	cell wall-associat
17	251	11.2	627	2 D75393	serine proteinase,
18	246.5	11.0	402	1 JU0332	alkaline proteinas
19	246.5	11.0	534	1 JS0173	alkaline proteinas
20	243	10.8	519	2 S71451	halolysin R4 (EC 3
21	242.5	10.8	401	2 I39974	serine proteinase
22	240	10.7	380	2 A49778	high-alkaline seri
23	240	10.7	488	2 A19130	proteinase [import
24	235.5	10.5	382	1 SUBSN	subtilisin (EC 3.4
25	235	10.5	378	2 A33973	high-alkaline seri
26	235	10.5	382	2 I39780	subtilisin (EC 3.4
27	234	10.4	910	2 C69456	subtilisin sendai
28	234	10.4	1374	2 D72593	hypothetical prote
29	232.5	10.3	525	2 G84406	halolysin [import

alkaline proteinas
subtilisin (EC 3.4
serine proteinase
streptococcal Csa
subtilisin like pr
subtilisin (EC 3.4
hypothetical prote
intraluminal subti
subtilisin (EC 3.4
subtilisin (EC 3.4
subtilisin (EC 3.4
alkaline proteinas
subtilisin (EC 3.4
halolysin (EC 3.4
serine proteinase

30 231 10.3 321 1 S27501
31 230.5 10.3 379 1 SUBSCL
32 229.5 10.2 601 2 JC4576
33 227 10.1 1167 1 A35066
34 226.5 10.1 1118 2 H97298
35 225.5 10.0 381 2 JH7298
36 225.5 10.0 613 2 JH5976
37 225.5 10.0 1052 2 T17093
38 223.5 9.9 381 1 SUBSI
39 223.5 9.9 381 1 SUBSS
40 223.5 9.9 381 2 JQ1487
41 222.5 9.9 275 2 JC1085
42 222 9.9 384 2 JC4802
43 221.5 9.9 272 2 A23624
44 221.5 9.9 530 2 A42605
45 221 9.8 1036 2 JC5568

RESULT 1
T18279
multidrug resistance transport protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18279
R:Shaulsky, G.; Loomis, W.F.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z18855
A:Accession: T18279
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1743 <SHA>
A:Cross-references: UNIPROT:Q23868; UNIPARC:UPI000013687D; EMBL:U60086; NID:g1399914; PIR
C:Genetics:
A:Gene: tagC

Query Match 23.3%; Score 523.5; DB 2; Length 1743;
Beat Local Similarity 27.9%; Pred. No. 3.5e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

QY 19 LYGQGIIVAVADTGLDTGR---NDS-----SMHEAFRGKITALYALGRTNANDTNGH 68
DB 314 LRKGQILUSIADTGLDGHCFSDSKYPIPLNSVNLNR-KVVTYITTSDDSKVDGH 372
QY 69 GTHVAGSVLG-----NGSTNKGMAPQANLVFQISMDSGGLGL---PSNLTQLFSQAY 119
DB 373 GTHICGSAAGTPEDSSVNISSFGLATDAKIAF---FDLASGSSSLTTPSDLKQLYQPLY 429
QY 120 SAGARIHNSWGA-----AVNGAYTTDSNRVDYVRKN-DMTILFAAGNEGPNGGTIS--A 172
DB 430 DAGARVHCDNSGVSVEGTGYSSTASIDDFLTPDFILRAAGN---NEQVLSLIT 486
QY 173 PGTAKNAITVGTATENLR-----PSFGSYADNI----- 199
DB 487 QSTAKNIVTGAHQTIHENYLTGDNINYOSSVDINQELICDFDSRYCNYTTAQCLES 546
QY 200 -----NHVAQFSRSGPTKDGRIKPDVMAQCTFTL 228
DB 547 NATGLASCCPTILRKSVIDAANTOPLYNENNICFSKSGPTHGGRKPKALVAFGEYIT 606
QY 229 SARSSLA-----PDSSFWANHSKYAYMGGTSMATPIVAGNVAQLREH-----F 272
DB 607 SARNSGANTTQCGDGLS-PTNALLA-IGSTSMATSFAAAAATTILRQVLDVGYVPTGSI 664
QY 273 VKNRGITPKPILLKALITAGA-----ADTGLGPNGN-----QWGRVT 311
DB 665 VESNKLQPTGSLKALMINNAQLLNGTFLQITSSSITYPSNQVFENFAGSLVQWGAIR 724
QY 312 LDKSINVAIVNNESS-----ADTGLGPNGN-----SLTSOKATVSEFT-- 338
DB 725 MSNWLHVNNNNNNNNNTSGITKFDGIGGLDLRLVKPNQWKEESLTGNTSICFTYK 784

ALIGNMENTS

A:Residues: 1-442 <KUN>
A:Cross-references: UNIPROT:O31788; UNIPARC:UPI000006043F; GB:Z99113; GB:AL009126; NID:9126
A:Experimental source: strain 168
C:Genetics:
F:146-398/Domain: subtilisin homology <SBT>
Query Match 14.3%; Score 320.5; DB 2; Length 442;
Best Local Similarity 29.7%; Pred. No. 4.4e-13;
Matches 107; Conservative 50; Mismatches 104; Indels 99; Gaps 16;
QY 11 DVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRNTNAN-----D 64
DB 136 EVVRNGQITLGGTVAVVDGTG-----YHPDLEGR-----IGFADMNQKTEPYD 183
QY 65 TNGHGTTHVAGSVLNGSTN-----KGMAPQANLVFOSIMDSGGGLGSLPSNLQTLFSQAYS 120
DB 184 DNGHGTGTCAGDVASSGASSGGYRGPAPANLIGKVLNKQS-GTLDIIIEGV----- 236
QY 121 AGARIHTNSWGAENV-----GAYTDSRNVDVVRKND-----MTIL 157
DB 237 -----EWCTQYNEEDNPEDIDIMSMGLGDALRYDHEQEDPLVRAVERAWSAGIVVC 288
QY 158 FAAGNEPNGGTISAPGTAKNAITVGTATENLRPSFGSYADNINHVAFSSRGPTKDGRIK 217
DB 289 VAAGNSGSDSQTIASFGVSEKVTIVGALDDNTA-----SSDDDTVASFSRGPTVYGKEK 344
QY 218 PDVMAPGTIFLSARSLSAPDSF-----WANHDSKIYAMGYSMTATPIVAGNVQALREHF 272
DB 345 PDILAPGVNIILRS-----PNSYIDKLQSRVSGSYFTMSGTSMATPICAGIAALILQ-- 399
QY 273 VKNRGITPK--PSLLKAALIAAGADIGLYPNGNQGWRTLDKSLNV---AYVNESSL 327
DB 400 -QNPDLTPDEVKELLK-----NGTDKW-----KDEDPNIYGAGVNAENS 439
RESULT 5
A1341
Microbial serine proteinase (EC 3.4.21.-), minor (vpr), precursor - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: A41341; B41341; S39700; D69730
R:Slomka, A.; Rufo Jr. G.A.; Theriault, K.A.; Dwyer, M.; Wilson, S.W.; Pero, J.
J. Bacteriol. 173, 6889-6895, 1991
A:Title: Cloning and characterization of the gene for an additional extracellular serine
A:Reference number: A41341; MUID:92041574; PMID:1938892
A:Accession: A41341
A:Molecule type: DNA
A:Residues: 1-806 <SLO>
A:Cross-references: UNIPROT:P29141; UNIPARC:UPI0000060C20; GB:M76590; NID:g143819; PIDN:
A:Accession: B41341
A:Molecule type: protein
A:Residues: 161-195 <SL2>
R:Glaser, P.; Kunst, F.; Arnaut, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu,
A.; Rapoport, G.; Danchin, A.
Mol. Microbiol. 10, 371-384, 1993
A:Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr
A:Reference number: S39655; MUID:95020537; PMID:7934828
A:Accession: S39700
A:Molecule type: DNA
A:Residues: 1-806 <GLA>
A:Cross-references: UNIPARC:UPI0000060C20; EMBL:X73124; NID:g413923; PIDN:CAA51601.1; PI
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bester
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, S.; Lardinols
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror,
keuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama, K
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69730
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-806 <KUN>
A:Cross-references: UNIPARC:UPI0000060C20; GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAI
A:Experimental source: strain 168
C:Comment: The amino terminal sequence of the mature protein and a molecular weight of or
C:Genetics:
A:Gene: vpr
A:Start codon: TTG
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-160/Domain: propeptide #status predicted <PRO>
F:180-548/Domain: subtilisin homology #status atypical <SBT>
Query Match 13.8%; Score 310.5; DB 2; Length 806;
Best Local Similarity 23.5%; Pred. No. 4.3e-12;
Matches 129; Conservative 58; Mismatches 157; Indels 205; Gaps 18;
QY 18 GLYGQGIIVAVADTGLDTR-----NDSSMHEAFRGKITALYALGRNTN 60
DB 177 GYTGKGIKVAIIDTGEYVNHDPDKKNGFYQGYDVPDNDYDPKPTG-----D 225
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAQANLVFOSIMDSGGGLGSLPSNLQTLFSQAYS 120
DB 226 PRGEATDHTGHVAGTVAANG-TIRGVAPDATTLLAYRVLGPGG--SGTTENVIAGVERAVQ 282
QY 121 AGARIHTNSWGAENVAYTDSRNVDVVRKNDMTILFAAGNEPNGGTISAPGTAKNAI 180
DB 283 DGADVMNLSLNSLNPNPDWATSTAL-DWAMSEGVAVVTSNGNSGNGVTSVSGPTISREAI 341
QY 181 TVGATE-----NLRPSFGSY----- 195
DB 342 SVGATQLPLNEVAVTFGSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKEKDFEGKOLT 401
QY 196 -----ADNI----- 199
DB 402 GKVAVVKGSIATFVDKADNAXKAGAGMVMVNNLSGEIEANVPGMVSPTIKLSLEDEKEL 461
QY 200 -----NHVAFSSRGPTKD-CRIKPDVMAPGTIFLSARSLSLAP 236
DB 462 VSALKAGETKTKTLTVSKALGEQVADFSSRGVPVNDTWIKPDISAPGVNIVSTIPTHDP 521
QY 237 DSSFWANHDSKIYAMGYSMTATPIVAGNVQALREHFVKNRGITPKPSL--LKAALIAGAA 294
DB 522 D-----HPYGVGSKQGTSMASPHIAGAVAIKQ-----AKPKWSVEQIKAAIMNTAV 568
QY 295 DI-----GLGYPNGNQGWRTLDKSLNVAYVNESSLSSTSKATYSFTATAGKPLKISLV 350
DB 569 TLKOSDGEVYPHNAQAGSARI-----MNAIKADSLVSPGSYSY-----GTFLEK----- 612
QY 351 WSDAPASTTASVTLVNDLVLITAPNGTQYVGNDFTSVNDNDWG--RNNVENVFVINAQ 408
DB 613 -ENGETNKETFTENQ-----SSIRKSYTLEYSFNGSGISISGTSRVVIPAQ 660
QY 409 SGTVTIEVQ 417
DB 661 TKGATAKVK 669
RESULT 6
T28159
pyrolysin (EC 3.4.-.-) - Pyrococcus furiosus
C:Species: Pyrococcus furiosus
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28159

R;Voorhorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, R.J.; Vos, J. Biol. Chem. 271, 20426-20431, 1996
A:Title: Isolation and characterization of the hyperthermostable serine protease, pyroly
A:Reference number: Z20481; MUID:96355370; PMID:8702780
A:Accession: T28159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1398 <VOO>
A:Cross-references: UNIPROT:P72186; UNIPARC:UPI000016FD59; EMBL:U55835; NID:g1556462; PI
A:Experimental source: DSM3638
C:Genetics:
C:Keywords: hydrolase; serine proteinase

Query Match 13.5%; Score 302.5; DB 2; Length 1398;
Best Local Similarity 26.6%; Pred. No. 2.9e-11;
Matches 139; Conservative 57; Mismatches 178; Indels 149; Gaps 22;

QY 21 GGGQIVAVADTGLDTRNDSS-----SMHEAFRGKITALLYALGRTNAN----- 63
DB 301 GNGYDIAYVDLDDYDFDEVPLGOYNTYDVAVFSYYGPLYVLAIEDPNGEYAVFGW 360

QY 64 DTNGHGTAVAGSVLNGSTN-----KGMAPQAN 91
DB 361 DGHGHTVAGTVAGYDSNNDAWDLMSYGEWVFSRLYGDYTNVTDTVQGVAPGAQ 420

QY 92 LVFQSIMDSGGGLGLPSNLQTLPSQAYSAGARIHTNSGVAINGAYT--TDSRN--VDD 147
DB 421 IMAIRVLR--DGRGSMWDIEGM--TYAATHGADVISMSLGG--NAPYLDGTDPSVAVDE 476

QY 148 YVRKNDMTILFAAGNEGPNGGTISAPGTAKNAITVGATENLRPSGSYAD----- 197
DB 477 LTEKGVVVFVAAGNEGGINVSGVATRAITVGAAA--VPINGVVVSQALGYPDYG 535

QY 198 -----NINHVAOFSRGPCKGRIPDVNAPGTFILSARSLAPDSSFWANHDSKYA 249
DB 536 FYFPAITNV--RIAPFSRGPRIIDGEIKPNVAPGYGIYSSLPMMIGGADF----- 585

QY 250 YMGTSMTPIVAGNVAQLREHFVNRGRTPKPSLLKAALTAGADI-----GLGYPNG 303
DB 586 --MSGTSMATPHVSGVVALLISG--PKPEGIYVNPDIKKVLESGATWLEGDPYTGOKYTEL 643

QY 304 NQGMGRVTLDKSLNVAIVYNESSLSQTSKATYSFTATAGKPLKISLVMSDAPASTTA--- 360
DB 644 DQGHGLNVTKSWEI-----LKAINGTTLPIVDHWDKSYSDFAEYL 685

QY 361 SVTLVNDLDLVTAPN-----GTYQYVGN-----DFTSPYNDNW-----DG-----RNVENVF 403
DB 686 GVDVIRGLYARNSIPDIVEMHIKYVGDTEYRTFEIYATEPWIKPFVSGSVILENNTFEVL 745

QY 404 -----INAPQSGTY-----TIEVOAYNVVPVGPQTF 429
DB 746 RVKYDVEGLEPLGYVGRIIDPTTFVIEDEILNTIPIPEKT 788

RESULT 7
S11890
serine proteinase (EC 3.4.21.-) precursor, extracellular - Xanthomonas campestris pv. ca
N:Alternate names: subtilisin-related proteinase
C:Species: Xanthomonas campestris pv. campestris
C:Date: 21-Nov-1993 #sequence_revision 07-Feb-1997 #text_change 31-Dec-2004
C:Accession: S11890
R:Liou, Y.N.; Tang, J.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J.
Mol. Gen. Genet. 220, 433-440, 1990
A:Title: A multipurpose broad host range cloning vector and its use to characterise an e
A:Reference number: S11890; MUID:90251253; PMID:2187155
A:Molecule type: DNA
A:Residues: 1-580 <LIU>
A:Cross-references: UNIPROT:P23314; UNIPARC:UPI000012A398; EMBL:X51635; NID:g48533; PIDN
A:Experimental source: Xanthomonas campestris pv. campestris
A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 3 in having 205-Ala
C:Superfamily: extracellular alkaline serine protease precursor, Alteromonas type

C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:168-423/Domain: subtilisin homology <SBT>

Query Match 12.6%; Score 283; DB 2; Length 580;
Best Local Similarity 26.2%; Pred. No. 1.5e-10;
Matches 127; Conservative 55; Mismatches 147; Indels 156; Gaps 24;

QY 21 GGGQIVAVADTGL-----DTGRNDSMEHAFRGKITALLYALGRTNAND----- 64
DB 168 GSGTVVAVIDGITSHADLNANILAGYDFISDAITARDGNGRDSNAADGDGWAANECA 227

QY 65 -----TNGHGTAVAGSVLNGSTNKGMAPOA-----NLVFSQIMD 99
DB 228 GIPAASSWHGTHVAGTVAAVTNNTTGVAGTAYGAKVVPVRLGKCGGSLSDIADAIVMA 287

QY 100 SGGGLGLPSNLQ--TLFSQAYSAGARIHTNSGVAINGAYTDSRNVDYVRKNDMTIL 157
DB 288 SGGTVSGIPANANPAEVINMSLGGGSCSTTQMN--AINGAVSRGT-----IVV 334

QY 158 FAAGNEGPNGGTISAPGTAKNAITVGATEN--LRPSFGSYADNINHVAQFSSRGPTKDR 215
DB 335 VAAGNDASNVSG--SLPANCANVIAVATTSAGAKASVNFGTGI----- 377

QY 216 IKPDVMAFGTIFLSARSS--LAPDSSFWANHDSKYAYMGTSMTAPIVAGNVAQLREHFV 273
DB 378 --DVSAPGSSILSTLNSGTTTPGS-----ASYASVNGTSMASPHVAGVVALVQS--V 425

QY 274 KNRGITPK--PSLLK--NALTAGAADIGLGVPNGNQGRVTLDKSLNVAIVNESS----- 325
DB 426 APTALTTPAAVETLLKNTARALPGAC-----SGCGGAGIVNADAATVAA--INGSGGGG 477

QY 336 -----SLTSQKATYSFTATAGKPLKISLVMSDAPASTTASVTL---VND 367
DB 478 GGGNTLNGTPTVGLGAATGAEILNYTITVPAG-----SGLTIVTTSGSGSD 523

QY 368 LDLVI---TAPNGTYQVGNDFTPSYNDNMGNNVNFVINAPOSGTGTIEVOAYNVVPV 424
DB 534 ADLYVRAGSAPTDAYT---CRPYRS-----GNAETCTITAP--SGTYVYVRLKAYS----- 569

QY 425 PQTF 429

DB 570 --TFS 572

RESULT 8

S25835

subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41)

C:Species: Bacillus sp.

C:Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C:Accession: S25835

R:Davail, S.; Feller, G.; Narinx, E.; Gerday, C.

Gene 119, 143-144, 1992

A:Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacillus
F:135-373/Domain: subtilisin homology <SBT>
F:144,184,359/Active site: Asp, His, Ser #status predicted

A:Accession: S25835

A:Molecule type: DNA

A:Residues: 1-419 <DAV>

A:Cross-references: UNIPARC:UPI00000BB77A; EMBL:X63533; NID:g40198; PIDN:CAA45096.1; PID:

C:Superfamily: Subtilisin; subtilisin homology

C:Keywords: extracellular protein; hydrolase; serine proteinase

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-110/Domain: propeptide #status predicted <PRO>

F:111-419/Product: microbial serine proteinase #status predicted <MAT>

F:135-373/Domain: subtilisin homology <SBT>

F:144,184,359/Active site: Asp, His, Ser #status predicted

Query Match

Best Local Similarity 33.0%; Score 281; DB 1; Length 419;

Matches 87; Conservative 38; Mismatches 97; Indels 42; Gaps 13;

QY 21 GGGQIVAVADTGLDTRNDSSMH--BAFRGKITALLYALGR-----NNANDTNGHTHVAGSV 76
DB 168 GSGTVVAVIDGITSHADLNANILAGYDFISDAITARDGNGRDSNAADGDGWAANECA 227

Db 135 GAGINIAVLDTGVNTHNPDLNNVECKD-----FTVGTNFTDNSCTDRQGHCTHVAGSA 189

QY 77 LGNGSTNK---GMAPQANL-VFQSIMDSGGGLG-GLPSNLQTLFQSAYSAGARIHTN-SW 130

Db 190 LANGGTGSGVYGVPAEADLWAYKVLGDGSGVADDAEAI RHAGDQATALTNTKVVINMSL 249

QY 131 GAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPCTAKNAITVGTATENLRP 190

Db 250 GSGGESSLIT---NAVYAYDKGLVLIIAAGNSGPKPGSIGYPGALVNVAVAALENTIQ 306

QY 191 SFGSYADNINHNAQFSRSGPTKDG-----RIKPDVMAFCTFTLSARSSSLAPDSSFWANH 244

Db 307 N-GTY-----RVADFSSRGHKRTAGDYVIQKGDVEISAFGAAYST-----W--F 348

QY 245 DSKYAVMGTSMATPIVAGNVAQL 268

Db 349 DGGYATISGTSMASPHAAGLAAKI 372

RESULT 9

G83753

subtilisin-type proteinase (EC 3.4.21.-) vpr precursor [similarity] - Bacillus haloduran

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: G83753

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: G83753

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-799 <STO>

A:Cross-references: UNIPROT:O9KEM1; UNIPARC:UPI00000C39DC; GB:AP001510; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: vpr

C:Superfamily: microbial serine proteinase vpr; subtilisin homology

C:Keywords: hydrolase; serine proteinase

F:1-29/Domain: signal sequence #status predicted <SIG>

Query Match 12.5%; Score 280; DB 2; Length 799;

Best Local Similarity 24.7%; Pred. No. 3.7e-10;

Matches 117; Conservative 50; Mismatches 135; Indels 172; Gaps 16;

QY 18 GLYGQGIIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTNANDT-----NGH 68

Db 171 GYTGEITVAILLDTGVDTYHPD--LVHAF-GDYKGWDFDNDNDPQETPPGDPGRGIEITH 227

QY 69 GTHVAGSLVNGSTNKGMAPQANLVPQSIMDSGGGLGGLPSNLQTLFQSAYSAGARIHTN 128

Db 228 GTHVAGTVAANGLI-KGVAPDANLLAYRVLGPG--RGSTAGVIAGIERAVQDGADIMNL 284

QY 129 SNGAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPCTAKNAITVGTATENL 188

Db 285 SLGNTLNDPDFATSTIAL-DWMAEGVAVTNSNGSGFNWTVGSPGTSRDAISVGAT---- 340

QY 189 RPSFGSY-----ADNINH----- 201

Db 341 RLPYNYKASVTSIGIDYPSADIMGFPDSDEHLELDGTYEVAFAGLKPGDFGVDE 400

QY 202 ----- 201

Db 401 GKIALIVRGEIIPFVEKAENAKAAGVAGIYNNVAGVQPTVPLATPTIMLSNEDGLKMR 460

QY 202 -----VAQFSRSGPT-KDGRIKPDVMAFGCTFILSARSLAPD 237

Db 461 NLENGQNTVTFPIEDKLVGTEVADFSSRGPPVMTWMIKPDVPSAPGVAIVSTIPTHQPD 520

QY 238 SSFWANHDSKYAVMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADT- 296

Db 521 DPT-----GYSGRQGTSMASPHVGAALLLLEAH-PWNGV-----DHVKAALMNTAENLV 569

QY 297 ---GLGYPNGNOGWRVTLDKSLNAVYVNESSLSLTSQKATY-SFTATAGKPLK 346

Db 570 DENGRIYPHNTQAG-----SIRIVDAIESETLVTPGSHSFGTFTTKERKQVE 617

RESULT 10

T29090

surface layer-associated STABLE proteinase - Staphylothermus marinus

N:Alternate names: hyperthermostable proteinase

C:Species: Staphylothermus marinus

C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C:Accession: T29090

R:Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.

Curr. Biol. 6, 739-749, 1996

A:Title: A hyperthermostable protease of the subtilisin family bound to the surface layer

A:Reference number: Z20559; MUID:96385442; PMID:8793300

A:Accession: T29090

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1345 <MAY>

A:Cross-references: UNIPROT:D54437; UNIPARC:UPI0000062778; EMBL:U57968; NID:gl374755; PII

A:Experimental source: strain F1

C:Function:

A:Description: probably serves an exodigestive function related to the organism's energy

A>Note: stoichiometric S-layer component

Query Match 12.4%; Score 279.5; DB 2; Length 1345;

Best Local Similarity 29.9%; Pred. No. 7.9e-10;

Matches 99; Conservative 45; Mismatches 106; Indels 81; Gaps 14;

QY 46 FRGKITALYALGRTNANDTNGHGHVHA-----GSVL-----GNGSTNK-GMAPQANLV 93

Db 445 YQGRYLAL-----VSDFHGHGTSVATVIASRGRLVLDYGDGKLYRIMGVAPGAKI- 495

QY 94 FQSIMDSGGGLGGLPSNLQTLFQSAYSAG-----EAWLGFNIVTBEEDGVYVLSLDPPFGPHRADIISNSW 546

Db 496 -----AGGDWILLGNLVL--EAWLGFNIVTBEEDGVYVLSLDPPFGPHRADIISNSW 546

QY 131 GAAVNGAYTTDSNRVD-----DYVRKNDMTILFAAGNEGPNGGTISAPGTAK 177

Db 547 GSIYINFMLQPPGIDYRSSFMDEILAIRNYLIGDHVTIVFAAGNEGPGYSSNGAPGTGL 606

QY 178 NAITVGATE-NLRSPFG---SYADNINHVAQFSRSGPTKDGRIKPDVMAFGCTFILSARS 232

Db 607 LVITAGASTLMDYTRIYGYPEGYAD---EVIPFSRSGPTGQGYPKPDIVNIGAFEWASTR 663

QY 233 SLAPDSSFWANHDSKYAVMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAG 292

Db 664 TI-DGRGYQAQPD----VFGGTSEATPYTSGTLALVFOAYKEVYNTTPDPVTAKIILKSS 718

QY 293 AADIGLGYPNQNGWRVTLDKSLNAVYVNE 323

Db 719 AKDI--WYPAPSQSGSRVDALKAAADTVFISE 747

RESULT 11

S23407

subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39)

C:Species: Bacillus sp.

C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004

C:Accession: S23407

R:Narinx, E.; Davail, S.; Feller, G.; Gerday, C.

Biochim. Biophys. Acta 1131, 111-113, 1992

A:Title: Nucleotide and derived amino acid sequence of the subtilisin from the antarctic

A:Reference number: S23407; MUID:92256481; PMID:1581352

A:Accession: S23407

A:Molecule type: DNA

A:Residues: 1-420 <NAR>

A:Cross-references: UNIPROT:P28842; UNIPARC:UPI0000136183; EMBL:X62369; NID:g40200; PIDN:

C:Genetics:

A:Gene: subtil

C:Superfamily: Subtilisin; subtilisin homology

C:Keywords: extracellular protein; hydrolase; serine proteinase

F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-111/Domain: propeptide #status predicted <PRO>
F:112-420/Product: microbial serine proteinase #status predicted <MAT>
F:136-374/Domain: subtilisin homology <SBT>
F:145,185,360/Active site: Asp, His, Ser #status predicted

Query Match 12.3%; Score 277; DB 1; Length 420;
Best Local Similarity 31.2%; Pred. No. 2.4e-10;
Matches 98; Conservative 44; Mismatches 120; Indels 52; Gaps 16;

QY 21 GGGQIVAVADTGLDTRNDSSMHEAFRGKITAL--YALGRT---NNANDTNGHGHVAGS 75
DB 136 GGGINIAVLDTGVTN-----HPDLNNVEQCKDFTVGTITYNNSTCTDRQGHGHVAGS 189
QY 76 VLNGSTNK--GMAPOANL-VFQSIMDSGGGLG-GLPSNLQTLFQSAVSAGARHTN-S 129
DB 190 ALADGGTNGVYGVAPDADLWAYKVLGGDGSYADIDAAAIRHAGDQATALNKTVVINNS 249
QY 130 MGAAVNGAYTDSNRVDDYVRKNDMTILFAAGNEPGNGGTISAPGTAKNAITVGATENLR 189
DB 250 LGSSGESSLITNAVN---YSYNGKVLIIAAGNSGPGYQSGIGYPCGALYNVAVAALEN-K 305
QY 190 PFGSYADININIVAFSSRGPT-KDG-----RIKPDVWAPGTFFLSARSSLAPDSSFWAN 243
DB 306 VENGTY-----RVADFSSRGYWTGDYAIQKGDVEISAPGAAYST-----W-- 348
QY 244 HPSKYVMGSGTSMATPIVAGNAQLREHFVKRGITPKPSLLKAAALAGAADIGLGPNG 303
DB 349 FDGGTATISGTSMAFPHAGLAALKIWAQYPSASNVDRGELQYRAY---ENDILSGYAG 405
QY 304 -----NQQMGRTVL 312
DB 406 YGDDPFASGFGFATV 419

RESULT 12
JC4908
alkaline serine proteinase (EC 3.4.-.-) I precursor - Alteromonas sp.
N:Alternate names: subtilase
C:Species: Alteromonas sp.
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 05-Oct-2004
C:Accession: JC4908
R:Tsujiibo, H.; Miyamoto, K.; Tanaka, K.; Kaidzu, Y.; Imada, C.; Okami, Y.; Inamori, Y.
Biosci. Biotechnol. Biochem. 60, 1284-1288, 1996
A:Title: Cloning and sequence analysis of a protease-encoding gene from the marine bacterium *Alteromonas* sp.
A:Reference number: JC4908; MUID:97141200; PMID:8987544
A:Accession: JC4908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-715 <TSU>
A:Cross-references: UNIPROT:P70765; UNIPARC:UPI000017A928; DBJ:D38600; NID:g1536787; PI
A:Experimental source: strain O-7
C:Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sensit
C:Genetics:
A:Gene: aprI
A:Superfamily: extracellular alkaline serine protease precursor, Alteromonas type
C:Keywords: hydrolase
F:1-40/Domain: signal sequence #status predicted <SIG>
F:41-150/Domain: amino-terminal propeptide #status predicted <ATP>
F:151-496/Product: alkaline serine protease I #status predicted <MAT>
F:182-452/Domain: subtilisin homology <SBT>
F:497-715/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:239-294,335-372,478-481/Disulfide bonds: #status predicted

Query Match 11.9%; Score 267; DB 2; Length 715;
Best Local Similarity 25.9%; Pred. No. 2.1e-09;
Matches 124; Conservative 51; Mismatches 168; Indels 136; Gaps 23;

QY 21 GGGQIVAVADTG-----LDTRNDSSMHEAFRGKITALYALGRNNAND-----TNG---- 67
DB 182 GGGVVAVLDGTGYRPHLDLDANILPGYDMISNTFVANDGARDNDARDPGDAVTRGCT 241
QY 68 -----HGTHVAG---SVLNGSTNKGMAPOANLVFQSIMDSGGGLG 108

DB 242 DSSGQVPRADQDSSWHGTHVAGTVAAVTNNGEGVAGVAYDAKVVPVRVL-----GKCGGLT 298
QY 109 SNLQTLFQSAVSAGARIHTNSWGAIV-----NGAYTDSNRVDDYVRKNDMTILFAAG 161
DB 299 SDIADGIIWASGGSDRVPANANPAVVINMSLGGGACSAITQNAINQARNNGTIVIIAAG 358
QY 162 NEGPNGGTISAPGTAKNAITVGAT--ENLRPSPFGSYADININIHVAQFSRSGPTKDGRIKPD 219
DB 359 NDNDNSANYN-PGNCNGVVNVASVGRDGSRAVYSNYGANI-----D 398
QY 220 VWAPGTFFLSARSSLAPDSSFWANHDS-----KYAYMGTSMATPIVAGNVAQLR-- 269
DB 399 VAAPG---GAQSFADDPEGILSTHNSGSGAPSNDSYHSQGSTMAAPHVAGVAALIKOA 454
QY 270 -----EHFVKN--RGITPKPSLLKAAALAGAADI--GLG-----YPNGNQMGRTVL 312
DB 455 KPSATPDEVEITLKNTRSPFAGSCNCGTGVVDAANAANEALGDVVTPTGN-----TL 508
QY 313 DKSLNVAYVNBSSSLTSQKATYSFTATAGKPLKISLVMSDAPASTTASVTL---VNLDL 369
DB 509 ED--GVAKTGLSGAAGSNQ--PFTFDVPAGK-----TNVTFTMSGGTGDAD 550
QY 370 LVITAPNGTQVGNDFTPYNDNDWGR-----NNVENFINAPQSGTYTIEVQAYNVVPG 424
DB 551 LYVKL--GSQ-----PTSSYDCRPYEGNAEVCSPFADAPQAGTYHVMIINGYKAYS 599

RESULT 13
A72647
probable surface layer-associated STABLE proteinase APE0607 - Aeropyrum pernix (strain KJ
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A72647
R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-Do, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72647
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1331 <KAW>
A:Cross-references: UNIPROT:Q9YEG9; UNIPARC:UPI000005DBF6; DBJ:AP000060; NID:G5104188; I
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0607

Query Match 11.7%; Score 263; DB 2; Length 1331;
Best Local Similarity 23.6%; Pred. No. 8.8e-09;
Matches 111; Conservative 65; Mismatches 158; Indels 136; Gaps 18;

QY 8 VKADVQSSYGLYGGQIVAVADTGLDTRNDSSMHE-AFRGKITALYA----- 55
DB 346 VYADLS-TAYLYF-----LKALSDTGMISGEPDPSLLDJSFADETPASYGSEVLARDFTGD 400
QY 56 -----LGRTNNAN-----DTNGH 68
DB 401 GVNDSAGALAGTWYDVGWLLTGESVNLGRLGFDYAGLVLPCLDPQGRWVSLYDTLAH 460
QY 69 GTHVAGSVLNGSTN-----KGMAPQANLVFQSIMDSGGGLGGLPNSNLQTLFQSA 118
DB 461 GTSVATVIASRGVFNGLGYIETSLRGVAPGAKIA-----AGGSP-----LINVFAQL 509
QY 119 YSAG-----ARIHTNSWG---AAVNGAYT---TDSNRVDDY-VRKNDMT 155
DB 510 FLSGFEQDPSPLNWVYTGHEHQVDVNNNSWGNYSIALRGLTGADDTATTEDIVSASGT 569
QY 156 ILFAAGNEPGNGGTISAPGTAKNAITVGATE--NLRPSPFGSYADININIHVAQFSRSGPTK 213
DB 570 IVHANGNGGFGYGTATTFGAGSLISVGASTLFDYRPFYGLYPSPGDGVISWSDRGP 629
QY 214 GRIPDVMWAPGTFILSARSSLAPDSSFWANHDSKYAYMGTSMATPIVAGNVAQLREHFV 273

[illegible]

```
Db      416 CSYTGSLSGPDYNF---QPNGTYYSFAGTHRAWLRGPACTDF-DLYLWRWDGSRWLT 471
QY      398 -----NVENVFINAPOSQTYTIEVQAYN 420
Db      472 VGSSTGPTSEESLSYSTAGTYLWRIYAYS 501
```

Search completed: April 7, 2006, 09:43:27
Job time : 42 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:41:20 ; Search time 82 Seconds
(without alignments)
2211.438 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIKADVQAQSSVGLV.....EVQYNNVPGPQTFLAIYN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap.*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2247	100.0	434	3	US-09-985-689A-1
2	2247	100.0	434	4	US-10-385-662-2
3	2247	100.0	434	4	US-10-456-479-2
4	2247	100.0	434	4	US-10-837-566-1
5	2247	100.0	434	5	US-10-820-712A-1
6	2247	100.0	434	5	US-10-820-714A-1
7	2247	100.0	640	3	US-09-920-954-6
8	2247	100.0	640	4	US-10-456-479-4
9	2247	100.0	640	4	US-10-784-870-6
10	2247	100.0	640	5	US-10-820-712A-3
11	2247	100.0	640	5	US-10-820-714A-3
12	2242	99.8	434	4	US-10-456-479-11
13	2242	99.8	434	5	US-10-820-712A-14
14	2242	99.8	434	5	US-10-820-714A-15
15	2242	99.8	640	3	US-09-920-954-8
16	2242	99.8	640	4	US-10-784-870-8
17	2191	97.5	434	3	US-09-985-689A-2
18	2191	97.5	434	4	US-10-456-479-10
19	2191	97.5	434	4	US-10-837-566-2
20	2191	97.5	434	5	US-10-820-712A-12
21	2191	97.5	434	5	US-10-820-714A-13
22	2183	97.2	639	3	US-09-920-954-4
23	2183	97.2	639	4	US-10-784-870-4
24	2155	95.9	639	3	US-09-920-954-1
25	2155	95.9	639	4	US-10-784-870-1
26	2155	95.9	640	3	US-09-920-954-2
27	2155	95.9	640	4	US-10-784-870-2

28	2143	95.4	434	3	US-09-985-689A-6	Sequence 6, Appli
29	2143	95.4	434	4	US-10-456-479-15	Sequence 15, Appli
30	2143	95.4	434	4	US-10-837-566-6	Sequence 6, Appli
31	2143	95.4	434	5	US-10-820-712A-22	Sequence 22, Appli
32	2143	95.4	434	5	US-10-820-714A-23	Sequence 23, Appli
33	2125.5	94.6	433	3	US-09-985-689A-7	Sequence 7, Appli
34	2125.5	94.6	433	4	US-10-456-479-16	Sequence 16, Appli
35	2125.5	94.6	433	4	US-10-837-566-7	Sequence 7, Appli
36	2125.5	94.6	433	5	US-10-820-712A-23	Sequence 23, Appli
37	2125.5	94.6	433	5	US-10-820-714A-24	Sequence 24, Appli
38	1998.5	88.9	433	3	US-09-985-689A-5	Sequence 5, Appli
39	1998.5	88.9	433	4	US-10-456-479-14	Sequence 14, Appli
40	1998.5	88.9	433	4	US-10-837-566-5	Sequence 5, Appli
41	1998.5	88.9	433	5	US-10-820-712A-20	Sequence 20, Appli
42	1998.5	88.9	433	5	US-10-820-714A-21	Sequence 21, Appli
43	1994.5	88.8	433	3	US-09-985-689A-3	Sequence 3, Appli
44	1994.5	88.8	433	4	US-10-456-479-12	Sequence 12, Appli
45	1994.5	88.8	433	4	US-10-837-566-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-985-689A-1

; Sequence 1, Application US/09985689A

; Publication No. US20030022351A1

; GENERAL INFORMATION:

; APPLICANT: HATADA, YUJI

; APPLICANT: OGAWA, AKINORI

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SATO, TSUYOSHI

; APPLICANT: ARAKI, HIROYUKI

; APPLICANT: SUMITOMO, NOBUYUKI

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHIISA

; TITLE OF INVENTION: Alkaline proteases

; FILE REFERENCE: 215483US0

; CURRENT APPLICATION NUMBER: US/09/985,689A

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: JP P2000-355166

; PRIOR FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: JP P2001-114048

; PRIOR FILING DATE: 2001-04-12

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 434

; TYPE: PRT

; ORGANISM: Bacillus sp.

; US-09-985-689A-1

Query Match 100.0%; Score 2247; DB 3; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171; Indels 0; Gaps 0;
Matches 434; Conservative 0; Mismatches 0;

QY 1 NDVARGIKADVQAQSSVGLVGGQIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60

Db 1 NDVARGIKADVQAQSSVGLVGGQIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60

QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIWDSGGGLGGLPSNLQTLFSQAYS 120

Db 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIWDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARHTHTNSGAAVNGAYTTDSRNVDVVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Db 121 AGARHTHTNSGAAVNGAYTTDSRNVDVVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKGRKIPDVMAPGTFILSRSSSLAPDSSF 240

Db 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKGRKIPDVMAPGTFILSRSSSLAPDSSF 240

QY 241 WANHDSKYVMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGADIGLY 300

us-10-820-714a-1.rapbm

Mon Apr 10 06:49:18 2006

```

301 PNGNQGWGRTVLDKSLNVAIVYNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
301 PNGNQGWGRTVLDKSLNVAIVYNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
361 SVTLVNDLVLVITAPNGTQVVGNDFTSPYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
361 SVTLVNDLVLVITAPNGTQVVGNDFTSPYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
421 VPVGPQTFSLAIVN 434
421 VPVGPQTFSLAIVN 434

RESULT 3
US-10-456-479-2
; Sequence 2, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TORU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700USO
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
; US-10-456-479-2

Query Match 100.0%; Score 2247; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANTDNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANTDNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGVATYDTSRNVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGVATYDTSRNVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFILSARSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFILSARSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNQGWGRTVLDKSLNVAIVYNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
DB 301 PNGNQGWGRTVLDKSLNVAIVYNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLVITAPNGTQVVGNDFTSPYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
DB 361 SVTLVNDLVLVITAPNGTQVVGNDFTSPYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
421 VPVGPQTFSLAIVN 434
421 VPVGPQTFSLAIVN 434

US-10-385-662-2
; Sequence 2, Application US/10385662
; Publication No. US20040002432A1
; GENERAL INFORMATION:
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: SAITO, KAZUHIRO
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: IZAWA, YOSHIFUMI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KOBAYASHI, TORU
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: Alkaline protease
; FILE REFERENCE: 234938USO
; CURRENT APPLICATION NUMBER: US/10/385,662
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: JP 2002-081428
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: JP 2002-165987
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: JP 2002-304230
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: JP 2002-304231
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
; US-10-385-662-2

Query Match 100.0%; Score 2247; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANTDNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANTDNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGVATYDTSRNVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGVATYDTSRNVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFILSARSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFILSARSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300

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Db 421 VVVGPTFSLAIVN 434
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RESULT 4
US-10-837-566-1
; Sequence 1, Application US/10837566
; Publication No. US20040203129A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NORIYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSURISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/10/837,566
; PRIOR FILING DATE: 2004-05-04
; PRIOR FILING DATE: US/09/985,689A
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-837-566-1

Query Match 100.0%; Score 2247; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAGSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAGSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFTLSARSSLPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFTLSARSSLPDSSF 240
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLY 300
Qy 301 PNGNQGWGRVTLDKSLNVAIVYVNESSLSSTQKATYSTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAIVYVNESSLSSTQKATYSTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQVGNDFTSYNDNDGRNNVENFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQVGNDFTSYNDNDGRNNVENFINAPQSGTYYTIEVOAYN 420
Qy 421 VVVGPTFSLAIVN 434
Db 421 VVVGPTFSLAIVN 434

RESULT 5
US-10-820-714a-1
; Sequence 1, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR FILING DATE: 2003-106708
; PRIOR APPLICATION NUMBER: 2003-106708
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-1

Query Match 100.0%; Score 2247; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAGSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAGSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFTLSARSSLPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFTLSARSSLPDSSF 240
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLY 300
Qy 301 PNGNQGWGRVTLDKSLNVAIVYVNESSLSSTQKATYSTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAIVYVNESSLSSTQKATYSTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQVGNDFTSYNDNDGRNNVENFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQVGNDFTSYNDNDGRNNVENFINAPQSGTYYTIEVOAYN 420
Qy 421 VVVGPTFSLAIVN 434
Db 421 VVVGPTFSLAIVN 434

RESULT 6
US-10-820-714a-1
; Sequence 1, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
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; FILE REFERENCE: 251697US0		; NUMBER OF SEQ ID NOS: 24	
; CURRENT APPLICATION NUMBER: US/10/820,714A		; SOFTWARE: PatentIn version 3.0	
; CURRENT FILING DATE: 2004-04-09		; SEQ ID NO 6	
; PRIOR APPLICATION NUMBER: 2003-106709		; LENGTH: 640	
; PRIOR FILING DATE: 2003-04-10		; TYPE: PRT	
; NUMBER OF SEQ ID NOS: 24		; ORGANISM: Bacillus sp.	
; SOFTWARE: PatentIn version 3.2		US-09-920-954-6	
; SEQ ID NO 1		Query Match	
; LENGTH: 434		Best Local Similarity 100.0%; Score 2247; DB 5; Length 434;	
; TYPE: PRT		Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
; ORGANISM: Bacillus sp. KSM-KP43			
US-10-820-714A-1			
Query Match		100.0%; Score 2247; DB 5; Length 434;	
Best Local Similarity 100.0%; Pred. No. 3.6e-171;			
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	60
DB	1	NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	60
QY	61	NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS	120
DB	61	NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS	120
QY	121	AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	180
DB	121	AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	180
QY	181	TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPTGTFILSARSLAPDSF	240
DB	181	TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPTGTFILSARSLAPDSF	240
QY	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY	300
DB	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY	300
QY	301	PNGNQWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLWSDAPASTTA	360
DB	301	PNGNQWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLWSDAPASTTA	360
QY	361	SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVENFINAPOSGTYYTIEVQAYN	420
DB	361	SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVENFINAPOSGTYYTIEVQAYN	420
QY	421	VPVGPQTFSIAIYN 434	
DB	421	VPVGPQTFSIAIYN 434	
RESULT 7		US-09-920-954-6	
; Sequence 6, Application US/09920954		; Publication No. US20020064854A1	
; GENERAL INFORMATION:			
; APPLICANT: TAKAIWA, MIKIO			
; APPLICANT: OKUDA, MITSUYOSHI			
; APPLICANT: SAEKI, KATSUHISA			
; APPLICANT: KUBOTA, HIROMI			
; APPLICANT: HITOMI, JUN			
; APPLICANT: KAGEYAMA, YASUSHI			
; APPLICANT: SHIKATA, SHITSUW			
; APPLICANT: NOMURA, MASAFUMI			
; TITLE OF INVENTION: ALKALINE PROTEASE			
; FILE REFERENCE: 0327-0832-0PCT			
; CURRENT APPLICATION NUMBER: US/09/920,954			
; CURRENT FILING DATE: 2001-08-03			
; PRIOR APPLICATION NUMBER: 09/509,814			
; PRIOR FILING DATE: 2000-04-06			
; PRIOR APPLICATION NUMBER: PCT/JP98/04528			
; PRIOR FILING DATE: 1998-10-07			
; PRIOR APPLICATION NUMBER: JP 9-274570			
; PRIOR FILING DATE: 1997-06-08			
Query Match		100.0%; Score 2247; DB 4; Length 640;	

; FILE REFERENCE: 251697US0		; NUMBER OF SEQ ID NOS: 24	
; CURRENT APPLICATION NUMBER: US/10/820,714A		; SOFTWARE: PatentIn version 3.0	
; CURRENT FILING DATE: 2004-04-09		; SEQ ID NO 6	
; PRIOR APPLICATION NUMBER: 2003-106709		; LENGTH: 640	
; PRIOR FILING DATE: 2003-04-10		; TYPE: PRT	
; NUMBER OF SEQ ID NOS: 24		; ORGANISM: Bacillus sp.	
; SOFTWARE: PatentIn version 3.2		US-09-920-954-6	
; SEQ ID NO 1		Query Match	
; LENGTH: 434		Best Local Similarity 100.0%; Score 2247; DB 3; Length 640;	
; TYPE: PRT		Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
; ORGANISM: Bacillus sp. KSM-KP43			
US-10-820-714A-1			
Query Match		100.0%; Score 2247; DB 3; Length 640;	
Best Local Similarity 100.0%; Pred. No. 6e-171;			
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	60
DB	207	NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	266
QY	61	NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS	120
DB	267	NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS	326
QY	121	AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	180
DB	327	AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	386
QY	181	TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPTGTFILSARSLAPDSF	240
DB	387	TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPTGTFILSARSLAPDSF	446
QY	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY	300
DB	447	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY	506
QY	301	PNGNQWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLWSDAPASTTA	360
DB	507	PNGNQWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLWSDAPASTTA	566
QY	361	SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVENFINAPOSGTYYTIEVQAYN	420
DB	567	SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVENFINAPOSGTYYTIEVQAYN	626
QY	421	VPVGPQTFSIAIYN 434	
DB	627	VPVGPQTFSIAIYN 640	
RESULT 8		US-10-456-479-4	
; Sequence 4, Application US/10456479		; Publication No. US20040072321A1	
; GENERAL INFORMATION:			
; APPLICANT: SATO, TSUYOSHI			
; APPLICANT: OKUDA, MITSUYOSHI			
; APPLICANT: TAKIMURA, YASUSHI			
; APPLICANT: SUMITOMO, NOBUYUKI			
; APPLICANT: NOMURA, MASAFUMI			
; APPLICANT: KOBAYASHI, TOHRU			
; TITLE OF INVENTION: ALKALINE PROTEASE			
; FILE REFERENCE: 2387000U50			
; CURRENT APPLICATION NUMBER: US/10/456,479			
; CURRENT FILING DATE: 2003-06-09			
; PRIOR APPLICATION NUMBER: JP 2002-186387			
; PRIOR FILING DATE: 2002-06-26			
; PRIOR APPLICATION NUMBER: JP 2002-304232			
; PRIOR FILING DATE: 2002-10-18			
; NUMBER OF SEQ ID NOS: 16			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 4			
; LENGTH: 640			
; TYPE: PRT			
; ORGANISM: Bacillus sp. KSM-KP43			
US-10-456-479-4			
Query Match		100.0%; Score 2247; DB 4; Length 640;	

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Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
    |||||
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
    |||||
QY 61 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
    |||||
Db 267 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326
    |||||
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
    |||||
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
    |||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 240
    |||||
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 446
    |||||
QY 241 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIIGLY 300
    |||||
Db 447 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIIGLY 506
    |||||
QY 301 PNGNCGWRVTLDKSLNAVYNESSLSSTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
    |||||
Db 507 PNGNCGWRVTLDKSLNAVYNESSLSSTSQKATYSFTATAGKPLKISLVMSDAPASTTA 566
    |||||
QY 361 SVTLVNDLVLITAPNGTYVGNDFSTPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
    |||||
Db 567 SVTLVNDLVLITAPNGTYVGNDFSTPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 626
    |||||
QY 421 VPVGPQTFSLAIVN 434
    |||||
Db 627 VPVGPQTFSLAIVN 640
    |||||

RESULT 9
US-10-784-870-6
; Sequence 6, Application US/10784870
; Publication No. US20040142837A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUMI
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/10/784,870
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-784-870-6

Query Match 100.0%; Score 2247; DB 4; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
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Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
    |||||
QY 61 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
    |||||
Db 267 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326
    |||||
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
    |||||
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
    |||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 240
    |||||
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 446
    |||||
QY 241 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIIGLY 300
    |||||
Db 447 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIIGLY 506
    |||||
QY 301 PNGNCGWRVTLDKSLNAVYNESSLSSTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
    |||||
Db 507 PNGNCGWRVTLDKSLNAVYNESSLSSTSQKATYSFTATAGKPLKISLVMSDAPASTTA 566
    |||||
QY 361 SVTLVNDLVLITAPNGTYVGNDFSTPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
    |||||
Db 567 SVTLVNDLVLITAPNGTYVGNDFSTPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 626
    |||||
QY 421 VPVGPQTFSLAIVN 434
    |||||
Db 627 VPVGPQTFSLAIVN 640
    |||||

RESULT 10
US-10-820-712A-3
; Sequence 3, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-3

Query Match 100.0%; Score 2247; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
    |||||
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
    |||||
QY 61 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
    |||||
Db 267 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326
    |||||
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
    |||||
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
    |||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 240
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Db 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSSLPADSSP 446
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKNRGITPKPSLLKAALIAGAADIGLY 506
Qy 301 PNGNQWGRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPKISLVMSDAPASTTA 360
Db 507 PNGNQWGRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPKISLVMSDAPASTTA 566
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 626
Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 11
US-10-820-714A-3
; Sequence 3, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697USO
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-3
Query Match 100.0%; Score 2247; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
Qy 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSSLPADSSP 240
Db 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSSLPADSSP 446
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKNRGITPKPSLLKAALIAGAADIGLY 506
Qy 301 PNGNQWGRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPKISLVMSDAPASTTA 360
Db 507 PNGNQWGRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 626
Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 12
US-10-456-479-11
; Sequence 11, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700USO
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP9865
US-10-456-479-11
Query Match 99.8%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSSLPADSSP 240
Db 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSSLPADSSP 240
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Qy 301 PNGNQWGRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPKISLVMSDAPASTTA 360
Db 301 PNGNQWGRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
Qy 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 13

US-10-820-712A-14
; Sequence 14, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-US0
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-712A-14

Query Match 99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSVADNINHVAQFSRRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSVADNINHVAQFSRRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300

QY 301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLVLVTAPNGTQYVGNDFTPYNDWDRNNVNFVINAPOSQGTITIEVQAYN 420
DB 361 SVTLVNDLVLVTAPNGTQYVGNDFTPYNDWDRNNVNFVINAPOSQGTITIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 14

US-10-820-714A-15
; Sequence 15, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasuehi
; APPLICANT: Sato, Tsuyoshi

; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697US0
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-714A-15

Query Match 99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSVADNINHVAQFSRRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSVADNINHVAQFSRRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300

QY 301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLVLVTAPNGTQYVGNDFTPYNDWDRNNVNFVINAPOSQGTITIEVQAYN 420
DB 361 SVTLVNDLVLVTAPNGTQYVGNDFTPYNDWDRNNVNFVINAPOSQGTITIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 15

US-09-920-954-8
; Sequence 8, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570

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; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-8

Query Match      99.8%; Score 2242; DB 3; Length 640;
Best Local Similarity 99.8%; Pred. No. 1.5e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NDVARGIVKADVAGSSGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db      207 NDVARGIVKADVAGSSGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266

Qy      61 NANDTNGHGTGVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQSQAYS 120
Db      267 NANDTNGHGTGVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQSQAYS 326

Qy      121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db      327 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy      181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKQGRIPKDVMAPGTFILSARSSSLAPDSSF 240
Db      387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKQGRIPKDVMAPGTFILSARSSSLAPDSSF 446

Qy      241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
Db      447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506

Qy      301 PNGNQGWGRVTLDKSLNVAIYVNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db      507 PNGNQGWGRVTLDKSLNVAIYVNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 566

Qy      361 SVTLVNDLDLVITAPNGIQYVGNDFTSYNDNWDGRNNVNFVINAPOSQTYTIEVQAYN 420
Db      567 SVTLVNDLDLVITAPNGIQYVGNDFTSYNDNWDGRNNVNFVINAPOSQTYTIEVQAYN 626

Qy      421 VPVGQTFESLAIVN 434
Db      627 VPVGQTFESLAIVN 640
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Search completed: April 7, 2006, 09:42:50
Job time : 83 secs

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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:42:58 ; Search time 83 Seconds
(without alignments)
163.100 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSVGLY.....EVQAYNVPVGPOTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New.*

- 1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	286.5	12.8	802	6	US-10-510-386-2		Sequence 2, Appli
2	253	11.3	874	6	US-10-510-386-28		Sequence 28, Appl
3	253	11.3	1047	6	US-10-510-386-200		Sequence 200, App
4	245	10.9	272	7	US-11-020-602-236		Sequence 236, App
5	240	10.7	269	7	US-11-020-602-6		Sequence 6, Appli
6	235.5	10.5	275	7	US-11-065-943-54		Sequence 54, Appl
7	235.5	10.5	275	7	US-11-020-602-3		Sequence 3, Appli
8	231.5	10.3	274	7	US-11-156-062-14		Sequence 14, Appl
9	230.5	10.3	274	7	US-11-156-062-12		Sequence 12, Appl
10	230.5	10.3	379	7	US-11-156-062-23		Sequence 23, Appl
11	229.5	10.2	274	7	US-11-020-602-5		Sequence 5, Appli
12	226.5	10.1	274	7	US-11-156-062-4		Sequence 4, Appli
13	226.5	10.1	274	7	US-11-156-062-8		Sequence 8, Appli
14	225.5	10.0	274	7	US-11-156-062-10		Sequence 10, Appl
15	225.5	10.0	1052	7	US-11-020-602-208		Sequence 208, App
16	224.5	10.0	274	7	US-11-156-062-6		Sequence 6, Appli
17	223.5	9.9	275	7	US-11-020-602-4		Sequence 4, Appli
18	221.5	9.9	274	7	US-11-156-062-16		Sequence 16, Appl
19	221.5	9.9	274	7	US-11-156-062-18		Sequence 18, Appl
20	220.5	9.8	274	7	US-11-156-062-2		Sequence 2, Appli
21	219.5	9.8	382	7	US-11-020-602-2		Sequence 209, App
22	209.5	9.3	280	7	US-11-020-602-209		Sequence 218, App
23	205	9.0	1432	6	US-10-510-386-218		Sequence 260, App
24	203	9.0	1647	7	US-11-052-554A-260		Sequence 24714, A
25	181	8.1	740	7	US-11-096-568A-24714		

26	181	8.1	777	7	US-11-096-568A-24713		Sequence 24713, A
27	181	8.1	790	7	US-11-096-568A-24712		Sequence 24712, A
28	177	7.9	591	6	US-10-510-386-22		Sequence 22, Appl
29	167	7.4	722	7	US-11-096-568A-31863		Sequence 31863, A
30	167	7.4	757	7	US-11-096-568A-31862		Sequence 31862, A
31	167	7.4	798	7	US-11-096-568A-31861		Sequence 31861, A
32	167	7.4	798	7	US-11-096-568A-17896		Sequence 17896, A
33	160	7.1	659	7	US-11-096-568A-17895		Sequence 17895, A
34	160	7.1	671	7	US-11-096-568A-17894		Sequence 17894, A
35	158.5	7.1	791	7	US-11-096-568A-24028		Sequence 24028, A
36	158.5	7.1	759	7	US-11-096-568A-24027		Sequence 24027, A
37	158.5	7.1	764	7	US-11-096-568A-24026		Sequence 24026, A
38	156	6.9	791	7	US-11-096-568A-31251		Sequence 31251, A
39	155	6.9	672	7	US-11-096-568A-23983		Sequence 23983, A
40	155	6.9	680	7	US-11-096-568A-23982		Sequence 23982, A
41	152.5	6.8	794	7	US-11-218-986-2		Sequence 2, Appli
42	152.5	6.8	820	6	US-10-821-234-1176		Sequence 1176, Ap
43	144.5	6.4	617	7	US-11-096-568A-31252		Sequence 31252, A
44	136.5	6.1	3132	7	US-11-087-099-1245		Sequence 1245, Ap
45	136	6.1	418	7	US-11-096-568A-23984		Sequence 23984, A

ALIGNMENTS

RESULT 1
US-10-510-386-2
; Sequence 2, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-2

Query Match	12.8%	Score 286.5;	DB 6;	Length 802;
Best Local Similarity	23.0%	Pred. No. 3.9e-13;		
Matches 143;	Conservative 69;	Mismatches 178;	Indels 231;	Gaps 27;
Qy	2	DVARGIVKADVAQSSVGLYGGQIVAVADTGLDTRND--SSMHAFRGK--ITALYALGR	58	
Db	158	DKSAPFGADQAWKS-GYTGKGIKVAIDTGVYTHPLKKNFGYKGYDFVNDYDQGE	216	
Qy	59	TNNANDTNG---HGTHVAGSVLGNSTNKGMAPQANLVFQSIMDSGGGLGSLPNSLQTLF	115	
Db	217	TPTGDPGCGATDHGTHVAGTTAANGQI-KGVAPEATLLAYRVLGPGG--SGTTENVIAGI	273	
Qy	116	SOAVSAGARIHTNSGAAVNGA-YTTDSRNVDYVKNDMTILFAAGNEGNGGTISARG	174	
Db	274	EKAVADGAKVMNLSLGNLSPDYATSI--ALDWAMAEVGVAVTNSNGSPENWTVGSPG	331	
Qy	175	TAKNAITVGTATE-----NLRPSFGS-----	194	
Db	332	TSRVAISVGSQOLPYNEYSVTLPSSYSSAKVMGYQEKLEALNGQEVLEAGLQADDF	391	
Qy	195	-----YADNINH-----	201	
Db	392	SGKDVKGKVAIQRGVIFPVDKAEAKNAGATGAIVYNNATGEIEANVMGMAVPTVKLSK	451	
Qy	202	-----VAQFSRSGPTKD--GRIKPDVWAPGTFILSA	230	

Db 452 EGEKLVQOIKEGKHSVVFSEFKLDKLGELTASFSRSGFVMDTWMKIPDVSAQVNIYST 511
QY 231 RSSLAPDSFWANHDSK-----YAYMGGTSMATPIVAGNVAQLREHFVKNRGITP--KPSL 284
Db 512 IPT-----HDPKPYGSGKQGTSMASPHVAGTAAILKQ-----AKPDWTPEQ 554
QY 285 LKAALIAGAADI-----GLGYPNGNGWGRVTLTDLKSLNAVYVNESS----- 326
Db 555 IKGVLMTAEKLTDENGKPLPHNTQAGSIRIMEALKASSIVTPGSHSYGTFKDKGKQT 614
QY 327-----LSTSQA-----TYSFTATAGKPLKISLVMSD---APASST---ASVTLYNDL 368
Db 615 KQAFTEIENLSHRKAYQLEYSFKGTG-----ITVSGTERVVVPANQTGKAAAKVTNSA 669
QY 369 DLVITAPNGTOVGNDFTSYNDNWDGRNNVE---NVFINAP-----QSGT 411
Db 670 KTKAGTYEGTVIRE-----DGRKVAEIPLLILVKEPDYPRVTSVTVPEGAKOGA 719
QY 412 YTIEVOAYNVVPGPTQFSLAI 432
Db 720 YTIE--AY-LPGAEELAPLV 737

RESULT 2
US-10-510-386-28
; Sequence 28, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-28

Query Match 11.3%; Score 253; DB 6; Length 874;
Best Local Similarity 27.2%; Pred. No. 1.2e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;
QY 25 IVAVADTGLDTRNDSSMHEAFRGKI---TALYALGRTNANDTNGHGTTHVAGSVLG--- 78
Db 447 VIAVDTGVHTLADLS-----GSVKDEGYNVGRGTADAMDDNGHGTTHVAGSVLG 500
QY 79 NGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYSAGARIHTNSWGAUVNGAY 138
Db 501 NHFSMAGINAYAKILPVKVLDSG--SGDTEQIANGIIYAADHGAKVINLSLG---GPY 554
QY 139 TTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAITVGATENLRPSFGSYADN 198
Db 555 SRVMEYALKYAASKNVTTIVAATGNDGVS--EISYPASSKYTLSVGATNNL----- 602
QY 199 INHVAQFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSFANHDSKYAYMGTSMAT 258
Db 603 -DLVSDYSNYGKGL-----DMVAPGTDI-----PSLVPDGN-----VTYMSGTMAA 643
QY 259 PIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGL---GYPNGN----- 304
Db 644 PHVAAAAGLL-----LSQNPSPKPKQIASLLTETTADVAFEEQDNPNPDYDLIDIEPAAQI 698
QY 305 -----QWGRVTLDKSLNAVYVNESSLSLTSQKATYSFTATAGKPLKI 347
Db 699 PGYDFVSGWGRNLNVFHAASVFELNMKVHPVLNRHTAVTGTAKSGVTVKI 747

RESULT 3
US-10-510-386-200
; Sequence 200, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-200

Query Match 11.3%; Score 253; DB 6; Length 1047;
Best Local Similarity 27.2%; Pred. No. 1.5e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;
QY 25 IVAVADTGLDTRNDSSMHEAFRGKI---TALYALGRTNANDTNGHGTTHVAGSVLG--- 78
Db 447 VIAVDTGVHTLADLS-----GSVKDEGYNVGRGTADAMDDNGHGTTHVAGSVLG 500
QY 79 NGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYSAGARIHTNSWGAUVNGAY 138
Db 501 NHFSMAGINAYAKILPVKVLDSG--SGDTEQIANGIIYAADHGAKVINLSLG---GPY 554
QY 139 TTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAITVGATENLRPSFGSYADN 198
Db 555 SRVMEYALKYAASKNVTTIVAATGNDGVS--EISYPASSKYTLSVGATNNL----- 602
QY 199 INHVAQFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSFANHDSKYAYMGTSMAT 258
Db 603 -DLVSDYSNYGKGL-----DMVAPGTDI-----PSLVPDGN-----VTYMSGTMAA 643
QY 259 PIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGL---GYPNGN----- 304
Db 644 PHVAAAAGLL-----LSQNPSPKPKQIASLLTETTADVAFEEQDNPNPDYDLIDIEPAAQI 698
QY 305 -----QWGRVTLDKSLNAVYVNESSLSLTSQKATYSFTATAGKPLKI 347
Db 699 PGYDFVSGWGRNLNVFHAASVFELNMKVHPVLNRHTAVTGTAKSGVTVKI 747

RESULT 4
US-11-020-602-236
; Sequence 236, Application US/11020602
; Publication No. US20060024764A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND METHODS OF MAKING AND USING THE SAME
; FILE REFERENCE: GC527C2
; CURRENT APPLICATION NUMBER: US/11/020.602
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 272
; TYPE: PRT

APPLICANT: Stehr, Regina
APPLICANT: Maurer, Karl-Heinz
TITLE OF INVENTION: SUBSTITUTED VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
FILE REFERENCE: HENK-0134 / H5698
CURRENT APPLICATION NUMBER: US/11/156,062
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: PCT/EP2003/014127
PRIOR FILING DATE: 2003-12-20
PRIOR APPLICATION NUMBER: DE 102 60 903.9
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23
LENGTH: 379
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-11-156-062-23

Query Match 10.3%; Score 230.5; DB 7; Length 379;
Best Local Similarity 30.2%; Pred. No. 1.7e-09;
Matches 85; Conservative 37; Mismatches 106; Indels 53; Gaps 11;
QY 7 IVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTNNDTN 66
DB 115 LIKADKVQAAQ-GFKGANVKVAVLDTGIAQASHPDLNVVGG-----ASFVAGEAYN-TDGN 166
QY 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYSAGAR 124
DB 167 GHGTHVAGTVAALDNTTGVGVAPSVLSYAVKVLNMSG--SGSYSGIVSGIEWATTNGMD 224
QY 125 IHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPN--GTISAPGTAKNAITV 182
DB 225 VINMSLGA---SGSTAMKQAVDNAYARGVVVAAAGNSGSGTNTTIGYPAKYDSVI 281
QY 183 GATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSSILAPDSSFWA 242
DB 282 GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 315
QY 243 NHDSKYAVMGTSMTATPIVAGNVA-----QLREHFVKNR 276
DB 316 ---NTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNR 353

RESULT 11
US-11-020-602-5
Sequence 5, Application US/11020602
Publication No. US20060024764A1
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GC597C2
CURRENT APPLICATION NUMBER: US/11/020,602
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 274
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-11-020-602-5

Query Match 10.2%; Score 229.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 1.4e-09;
Matches 85; Conservative 37; Mismatches 106; Indels 53; Gaps 11;
QY 7 IVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTNNDTN 66

DB 10 LIKADKVQAAQ-GFKGANVKVAVLDTGIAQASHPDLNVVGG-----ASFVAGEAYN-TDGN 61
QY 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYSAGAR 124
DB 62 GHGTHVAGTVAALDNTTGVGVAPSVLSYAVKVLNMSG--SGSYSGIVSGIEWATTNGMD 119
QY 125 IHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPN--GTISAPGTAKNAITV 182
DB 120 VINMSLGA---SGSTAMKQAVDNAYARGVVVAAAGNSGSGTNTTIGYPAKYDSVI 176
QY 183 GATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSSILAPDSSFWA 242
DB 177 GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 210
QY 243 NHDSKYAVMGTSMTATPIVAGNVA-----QLREHFVKNR 276
DB 211 ---NTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNR 248

RESULT 12
US-11-156-062-4
Sequence 4, Application US/11156062
Publication No. US20050281773A1
GENERAL INFORMATION:
APPLICANT: Wieland, Susanne
APPLICANT: Polanyi-Bald, Laura
APPLICANT: Prueser, Inken
APPLICANT: Stehr, Regina
TITLE OF INVENTION: SUBSTITUTED VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
FILE REFERENCE: HENK-0134 / H5698
CURRENT APPLICATION NUMBER: US/11/156,062
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: PCT/EP2003/014127
PRIOR FILING DATE: 2003-12-20
PRIOR APPLICATION NUMBER: DE 102 60 903.9
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 274
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-11-156-062-4

Query Match 10.1%; Score 226.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 2.3e-09;
Matches 85; Conservative 36; Mismatches 107; Indels 53; Gaps 11;
QY 7 IVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTNNDTN 66
DB 10 LIKADKVQAAQ-GFKGANVKVAVLDTGIAQASHPDLNVVGG-----ASFVAGEAYN-TDGN 61
QY 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYSAGAR 124
DB 62 GHGTHVAGTVAALDNTTGVGVAPSVLSYAVKVLNMSG--SGSYSGIVSGIEWATTNGMD 119
QY 125 IHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPN--GTISAPGTAKNAITV 182
DB 120 VINMSLGA---SGSTAMKQAVDNAYARGVVVAAAGNSGSGTNTTIGYPAKYDSVI 176
QY 183 GATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSSILAPDSSFWA 242
DB 177 GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 210
QY 243 NHDSKYAVMGTSMTATPIVAGNVA-----QLREHFVKNR 276
DB 211 ---NTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNR 248

RESULT 13

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US-11-156-062-8
; Sequence 8, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITUIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156,062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-8

Query Match      10.1%; Score 226.5; DB 7; Length 274;
Best Local Similarity 29.5%; Pred. No. 2.3e-09;
Matches 85; Conservative 36; Mismatches 100; Indels 67; Gaps 12;

Qy 7 IVKADVAQSSYGLYGQGGQIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTNANDTN 66
Db 10 LIKADKVAQ-GFGKANVAVLDGTGQASHPDLNVVG-----ASFVAGEAYNA-DGN 61
Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDS--GGGLGGLPSNLQTLFSQ----- 117
Db 62 GHGTHVAGTVAALDNTTGVLGVAPEVSVLYAVKVLNLSGSGSYSGVSGIEWATINDMDVI 121
Qy 118 AYSAGARIHTNSWGAANGAYTDSRNVDVVRKNDMTILFAAGNEGPNG--GTISAPGT 175
Db 122 NMSLGGASGSTAMKQAVDNAYA-----RGVVVAAAGNSGSGGNTNTIGYPAK 169
Qy 176 AKNATTCATENLRSPFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILSARSLA 235
Db 170 YDSVIAVGA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT-- 210
Qy 236 PDSFPAWHDSKYAYMGTSMTPIVAGNVA-----QLREHFVKNR 276
Db 211 -----NTYATWGTSMASPHVAGAAALILSKHPNLSASQVRNR 248

RESULT 14
US-11-156-062-10
; Sequence 10, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITUIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156,062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10

Query Match      10.0%; Score 225.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 2.7e-09;
Matches 85; Conservative 36; Mismatches 107; Indels 53; Gaps 11;

Qy 7 IVKADVAQSSYGLYGQGGQIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTNANDTN 66
Db 10 LIKADKVAQ-GFGKANVAVLDGTGQASHPDLNVVG-----ASFVAGEAYNA-DGN 61
Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDS--GGGLGGLPSNLQTLFSQAYSAGAR 124
Db 62 GHGTHVAGTVAALDNTTGVLGVAPEVSVLYAVKVLNLSG--SGSYSGVSGIEWATINDMD 119
Qy 125 IHTNSWGAANGAYTDSRNVDVVRKNDMTILFAAGNEGPNG--GTISAPGTAKNAITV 182
Db 120 VINMSLGA---SGSTAMKQAVDNAYARGVVVAAAGNSGSGGNTNTIGYPAKYSVIAV 176
Qy 183 GATENLRSPFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILSARSLAPDSSFWA 242
Db 177 GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 210
Qy 243 NHDSKYAYMGTSMTPIVAGNVA-----QLREHFVKNR 276
Db 211 ---NTYATWGTSMASPHVAGAAALILSKHPNLSASQVRNR 248

RESULT 15
US-11-020-602-208
; Sequence 208, Application US/11020602
; Publication No. US20060024764A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; FILE REFERENCE: GC527C2
; CURRENT APPLICATION NUMBER: US/11/020,602
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-020-602-208

Query Match      10.0%; Score 225.5; DB 7; Length 1052;
Best Local Similarity 26.7%; Pred. No. 1.5e-08;
Matches 117; Conservative 66; Mismatches 157; Indels 99; Gaps 26;

Qy 8 VKADVAQSSYGLYGQGGQIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTNAN----- 63
Db 197 LQADVLM-QMGYTCANVRVAVFDTGL-----SEKHPHFKN-----VKRTNNTNERTL 243
Qy 64 -DTNGHGTHVAGSVLNGSTNKGMAPOANLVFQSIMDS--GGGLGGLPSNLQTLFSQAYS 121
Db 244 DDGLGHGTFVAG-VIASMRECOGFPAPDAELHIFRVFTNN-----QVSYTSWFLDAFNY 295
Qy 122 GARIHTNSWGAANGAYTDSRNVDY--VRKNDMTILFAAGNEGPNGGTISAPGTAKNA 179
Db 296 AILKKIDVLNLSIGGPDFMDHPFVDKRWELTANNVIMVSAIGNDGPGLYGLTNLPADQMDV 355
Qy 180 ITVGATENLRSPFGSYADNINHVAQFSSRG-----PTKDGRIPDVMAFGTILSARSS 233
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Db	IGVGID-----PEDNI---ARFSSRGMTTWELPGGYGRMKPDIV---TYGAGVRS	401
Qy	LAPDSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGA	293
Db	GKGGC-----RALSGTSVASPVVAGAVTLLVSTVQKRELV--NPASMKQALIASA	450
Qy	ADIGLYPNGN--OGWGRVTLDKSLNV--AYVNESSLSLTS-----QKATYSFTATAGKP	344
Db	RRLL-----PGVNMFEQGHGKDLLRAYQILNSY--KQASLSPSYIDLTECPYMW-PYCSQP	504
Qy	LKISLWSDAPASTTASVTLVNDL---VITAPNGTQYVGNDFTSFYNDNWDGRNNVEN	401
Db	-----IYGGMP--TVVNTILNGMGVYGRIVDKPDWQPYL-----PQNG-----DNIEV	547
Qy	VF-----INAPQSGTYTIEV	416
Db	AFSYSSVLWFWGSLAISI	566

Search completed: April 7, 2006, 09:44:54
Job time : 84 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:27:45 ; Search time 91 Seconds
(without alignments)
2050.434 Million cell updates/sec

Title: US-10-820-714A-1-HIS15
Perfect score: 2251
Sequence: 1 NDVARGIVKADVAQHSYGLY.....EVQAYNPVGPQTFFSLAIVN 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2248	99.9	434	8	Adsl4438 Bacillus
2	2247	99.8	434	8	Adsl14439 Bacillus
3	2242	99.6	434	5	Aam50080 Bacillus
4	2242	99.6	434	7	Ady33778 Bacillus
5	2242	99.6	434	7	Adz51757 Wild-type
6	2242	99.6	434	8	Adl25802 Bacillus
7	2242	99.6	434	8	Adm40771 Mature al
8	2242	99.6	434	8	Adsl14427 Bacillus
9	2242	99.6	434	8	Adt49604 Bacillus
10	2242	99.6	640	2	Aay17090 Bacillus
11	2242	99.6	640	8	Adm40773 Alkaline
12	2242	99.6	640	8	Adsl4437 Bacillus
13	2242	99.6	641	8	Adt49613 Bacillus
14	2239	99.5	434	8	Adsl14443 Bacillus
15	2237	99.4	434	8	Adm40780 Alkaline
16	2237	99.4	434	8	Adsl14441 Bacillus
17	2237	99.4	640	2	Aay17091 Bacillus
18	2234	99.2	434	8	Adsl14444 Bacillus
19	2234	99.2	434	8	Adsl14442 Bacillus
20	2237	99.8	434	8	Adsl14440 Bacillus
21	2219	98.6	434	8	Adsl14445 Alkaline
22	2190	97.3	436	8	Adm40787 Bacillus
23	2186	97.1	434	5	Aam50081 Bacillus
24	2186	97.1	434	7	Adz51758 Mutant Ba

25	2186	97.1	434	8	Adm40779
26	2178	96.8	639	2	Aay17089
27	2150	95.5	639	2	Aay17087
28	2150	95.5	640	2	Aay17088
29	2138	95.0	434	5	Aam50085
30	2138	95.0	434	7	Adz51762
31	2138	95.0	434	8	Adm40784
32	2130.5	94.6	433	8	AdS52078
33	2130.5	94.6	433	8	AdS52011
34	2129.5	94.6	433	8	AdS52082
35	2126.5	94.5	433	8	AdS52083
36	2125.5	94.4	433	5	Aam50086
37	2125.5	94.4	433	7	Adz51763
38	2125.5	94.4	433	8	Adm40785
39	2125.5	94.4	433	8	AdS52010
40	2125.5	94.4	433	8	AdS52016
41	2125.5	94.4	433	8	AdS52001
42	2125.5	94.4	641	2	Aaw89547
43	2123.5	94.3	433	8	AdS52062
44	2123.5	94.3	433	8	AdS52054
45	2122.5	94.3	433	8	AdS52087

ALIGNMENTS

RESULT 1
ADSl4438
ID ADS14438 standard; protein; 434 AA.
XX
AC ADS14438;
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43 S15H/S16T mutant.
XX
KW protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;
mutin.
XX
OS Bacillus sp.; KSM-KP43.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 15 /note= "Wild-type Ser substituted by His"
FT Misc-difference 16 /note= "Wild-type Ser substituted by Thr"
XX
PN EP1466962-Al.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008604.
XX
PR 10-APR-2003; 2003JP-00106709.
XX
PA (KAOS) KAO CORP.
XX
PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
XX
DR WPI; 2004-711313/70.
XX
PT New engineered alkaline protease, useful particularly in laundry
detergents, comprising specified amino acids at particular positions.
XX
PS Example 1; Page; 31pp; English.
XX
CC The invention relates to a novel alkaline protease. The new alkaline
protease comprises an amino acid sequence in which one or more amino acid
residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
15 (histidine), position 16 (threonine or glutamine), position 166
(glycine), position 167 (valine), position 187 (serine), position 346

XX
AC AAM50080;
XX
DT 12-AUG-2002 (first entry)
XX
DE Bacillus sp KSM-KP43 alkaline protease protein fragment.
XX
DE Alkaline protease; detergent; laundry; bleaching; dishwasher.
XX
KW Bacillus sp.
XX
OS EP1209233-A2.
XX
PN 29-MAY-2002.
XX
PD 22-NOV-2001; 2001EP-00127851.
XX
PF 22-NOV-2000; 2000JP-00355166.
XX
PR 12-APR-2001; 2001JP-00114048.
XX
PA (KAOS) KAO CORP.
XX
PI Hatada Y, Ogawa A, Kageyama Y, Sato T, Araki H, Sumitomo N;
PI Okuda M, Saeki K;
XX
XX WPI; 2002-437518/47.
XX
DR New modified alkaline proteases useful in detergent compositions.
XX
XX Claim 1; Page 10-11; 25pp; English.
XX
CC This invention describes novel Bacillus sp. alkaline proteases useful in
CC detergent compositions, especially in laundry, bleaching or automatic
CC dishwasher detergents. The novel proteases have an increased detergency %
CC (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This
CC sequence represents a fragment of the alkaline protease KP43 from
CC Bacillus sp strain KSM-KP43 which is used to create the modified protease
CC represented in AAM50090
XX
SQ Sequence 434 AA;
Query Match 99.6%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAHVNGAYTTDSNRNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAHVNGAYTTDSNRNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPFGSYADNHNHVAQFSRGTGDKRIKPDVMAFGTPILSARSLAPDSF 240
DB 181 TVGATENLRPFGSYADNHNHVAQFSRGTGDKRIKPDVMAFGTPILSARSLAPDSF 240
QY 241 WANHSKYAYMGTSMTATPIVAGNVQAQLREHFVKNRGIPTKPSLLKAALIAGAADIGLY 300
DB 241 WANHSKYAYMGTSMTATPIVAGNVQAQLREHFVKNRGIPTKPSLLKAALIAGAADIGLY 300
QY 301 PNGNQGWGRTVLDKSLNVAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB 301 PNGNQGWGRTVLDKSLNVAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
QY 361 SVTLVNDLVLVTAPNGTQVGNDFTSYVNDNWDGRNNVFNAPQSGTGTITIEVQAYN 420
DB 361 SVTLVNDLVLVTAPNGTQVGNDFTSYVNDNWDGRNNVFNAPQSGTGTITIEVQAYN 420

QY 421 VPVGPOTFSLAIWN 434
DB 421 VPVGPOTFSLAIWN 434
RESULT 4
ADY33778
ID ADY33778 standard; protein; 434 AA.
XX
AC ADY33778;
XX
DT 05-MAY-2005 (first entry)
XX
DE Bacillus species alkaline protease.
XX
DE mutagenesis; alkaline protease; detergent; laundry; cosmetic; food;
KW bleaching detergent.
XX
OS Bacillus sp.
XX
PN EP1347044-A2.
XX
PD 24-SEP-2003.
XX
PF 21-MAR-2003; 2003EP-00006472.
XX
PR 22-MAR-2002; 2002JP-00081428.
XX
PR 06-JUN-2002; 2002JP-00165987.
XX
PR 18-OCT-2002; 2002JP-00304230.
XX
PR 18-OCT-2002; 2002JP-00304231.
XX
PA (KAOS) KAO CORP.
XX
PI Okuda M, Sato T, Saito K, Sumitomo N, Izawa Y, Saeki K;
PI Kobayashi T, Nomura M;
XX
XX WPI; 2003-846540/79.
DR N-PSDB; ADY33779.
XX
XX New alkaline protease having specific amino acid residue at a specific
PT position of its amino acid sequence, useful for producing detergent
PT compositions, laundry detergent, fiber modifiers, leather-treating agents
PT or pipe cleaners.
XX
PS Claim 1; SEQ ID NO 1; 31pp; English.
XX
CC The invention relates to an alkaline protease having a fully defined
CC sequence of 434 amino acids (I) given in the specification, or an amino
CC acid sequence at least 80% homology with (I), where an amino acid residue
CC at position 65, 101, 163, 170, 171, 273, 320, 359 or 387 of (I) is
CC selected from 16 amino acid residues. The amino acid residues at the
CC corresponding positions are selected from: position 65: proline; position
CC 101: asparagine; position 163: histidine, aspartic acid, phenylalanine,
CC lysine, asparagine, serine, isoleucine, leucine, glutamine, threonine or
CC valine; position 170: valine or leucine; position 171: alanine, glutamic
CC acid, glycine or threonine; position 273: isoleucine, glycine or
CC threonine; position 320: phenylalanine, valine, threonine, leucine,
CC isoleucine or glycine; position 359: serine, leucine, valine, isoleucine
CC or glutamic acid; and position 387: alanine, lysine, glutamine, glutamic
CC acid, arginine or histidine. The alkaline protease is useful for the
CC production of a detergent composition, such as laundry detergent, fiber
CC modifiers, leather-treating agents, cosmetic compositions, bath
CC additives, food modifiers and pharmaceutical compositions. The alkaline
CC protease may also be used as bleaching detergent, hard surface cleaning
CC detergent, pipe cleaner, artificial tooth cleaner, and as a sterilizing
CC cleanser for medical tools. The new alkaline protease has a more potent
CC proteolytic capacity, exhibiting excellent detergency for the removal of
CC a complex stain, and has high secretion capacity. This sequence
XX corresponds to the Bacillus sp. alkaline protease.
SQ Sequence 434 AA;

Query Match 99.6%; Score 2242; DB 7; Length 434;

PR	06-JUN-2002; 2002JP-001A5950.
XX	(KAOS) KAO CORP.
PA	WPI; 2004-0942297/10.
DR	N-PSDB; ADL25803.
XX	Novel mutant alkaline protease produced by substituting the amino acid residues useful as washing agent.
PT	Claim 1; SEQ ID NO 1; 21pp; Japanese.
XX	The invention comprises a mutant Bacillus alkaline protease which contains substitutions at positions 163, 170 and 434. The mutant alkaline protease is useful as a washing agent. The present amino acid sequence represents a Bacillus alkaline protease of the invention.
CC	Sequence 434 AA;
SQ	Query Match 99.6%; Score 2242; DB 8; Length 434; Best Local Similarity 99.8%; Pred. No. 1.5e-159; Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 NDVARGIVKADVAQHSHSYGLYGOGQIVAVADTGLDGRNDSSMHEAFRGKITALVALGRTN 60
Db	1 NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDGRNDSSMHEAFRGKITALVALGRTN 60
QY	61 NANDTNHGHGTTHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTILFSOAYS 120
Db	61 NANDTNHGHGTTHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTILFSOAYS 120
QY	121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db	121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY	181 TVGATENLRPSFGSYADNINHVAFQSSRGPDKGRIKPDVNPAGTFTILSARSSLAPDSSF 240
Db	181 TVGATENLRPSFGSYADNINHVAFQSSRGPDKGRIKPDVNPAGTFTILSARSSLAPDSSF 240
QY	241 WANHDSKYAYMGTSMATPIVAGNVQAQLREHFVKNRGITTPKPSLLKAALTAGAADIGLY 300
Db	241 WANHDSKYAYMGTSMATPIVAGNVQAQLREHFVKNRGITTPKPSLLKAALTAGAADIGLY 300
QY	301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTSOKATYSFTATAGKPKLSLVMSDAPASTTA 360
Db	301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTSOKATYSFTATAGKPKLSLVMSDAPASTTA 360
QY	361 SVTLVNDLDLVITAPNGTQYVGNDFTSPYNWDGRNNVENVFNAPOSQGYTTIEVOAYN 420
Db	361 SVTLVNDLDLVITAPNGTQYVGNDFTSPYNWDGRNNVENVFNAPOSQGYTTIEVOAYN 420
QY	421 VPVGPQTFLSAIVN 434
Db	421 VPVGPQTFLSAIVN 434
RESULT 7	
ADM40771	ID ADM40771 standard; protein; 434 AA.
XX	ADM40771;
DT	01-JUL-2004 (first entry)
XX	Mature alkaline protease from Bacillus sp. KSM-KP43.
DE	alkaline protease; laundry detergent; bleaching agent; detergent;
KW	denture-cleaning agent; enzyme.
XX	Bacillus sp.; KSM-KP43.
OS	US2004072321-A1.
PN	
XX	

PD	15-APR-2004.
XX	09-JUN-2003; 2003US-00456479.
PF	26-JUN-2002; 2002JP-00186387.
XX	18-OCT-2002; 2002JP-00304232.
PR	(KAOS) KAO CORP.
XX	Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
PI	WPI; 2004-328572/30.
XX	N-PSDB; ADM40772.
DR	New alkaline protease having a mutant prepro sequence where amino acid residues at positions 52, 75 and 142 are substituted with another amino acid residue, useful as enzyme component of laundry detergents, or bleaching agents.
XX	Claim 1; SEQ ID NO 2; 29pp; English.
PS	The invention relates to an alkaline protease having a prepro sequence. The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino acid residues at: (a) position 52 is substituted by aspartic acid or arginine; (b) position 75 is substituted by alanine or arginine; and (c) position 142 is substituted by lysine. The alkaline protease is useful as an enzyme which can be incorporated into laundry detergents, denture-cleaning agents, and detergents for sterilising medical apparatus. The present sequence represents mature alkaline protease from Bacillus sp. KSM-KP43.
CC	Sequence 434 AA;
XX	Query Match 99.6%; Score 2242; DB 8; Length 434; Best Local Similarity 99.8%; Pred. No. 1.5e-159; Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDGRNDSSMHEAFRGKITALVALGRTN 60
Db	1 NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDGRNDSSMHEAFRGKITALVALGRTN 60
QY	61 NANDTNHGHGTTHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTILFSOAYS 120
Db	61 NANDTNHGHGTTHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTILFSOAYS 120
QY	121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db	121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY	181 TVGATENLRPSFGSYADNINHVAFQSSRGPDKGRIKPDVNPAGTFTILSARSSLAPDSSF 240
Db	181 TVGATENLRPSFGSYADNINHVAFQSSRGPDKGRIKPDVNPAGTFTILSARSSLAPDSSF 240
QY	241 WANHDSKYAYMGTSMATPIVAGNVQAQLREHFVKNRGITTPKPSLLKAALTAGAADIGLY 300
Db	241 WANHDSKYAYMGTSMATPIVAGNVQAQLREHFVKNRGITTPKPSLLKAALTAGAADIGLY 300
QY	301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTSOKATYSFTATAGKPKLSLVMSDAPASTTA 360
Db	301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTSOKATYSFTATAGKPKLSLVMSDAPASTTA 360
QY	361 SVTLVNDLDLVITAPNGTQYVGNDFTSPYNWDGRNNVENVFNAPOSQGYTTIEVOAYN 420
Db	361 SVTLVNDLDLVITAPNGTQYVGNDFTSPYNWDGRNNVENVFNAPOSQGYTTIEVOAYN 420
QY	421 VPVGPQTFLSAIVN 434
Db	421 VPVGPQTFLSAIVN 434
RESULT 8	

RESULT 8

ADS14427
ID ADS14427 standard; protein; 434 AA.
XX
AC ADS14427;
XX
XX
DT 30-DEC-2004 (first entry)
DE
DE Bacillus alkaline protease KP43 mature protein SEQ ID NO:1.
XX
XX protease; enzyme; alkaline protease; laundry detergent; KP43.
XX
XX Bacillus sp.; KSM-KP43.
XX
XX EPI1466962-A1.
XX
XX 13-OCT-2004.
XX
XX 08-APR-2004; 2004EP-00008604.
XX
XX 10-APR-2003; 2003JP-00106709.
XX
XX (KAOS) KAO CORP.
XX
XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
PI
DR WPI; 2004-711313/70.
DR N-PSDB; ADS14428.
XX
XX
PT New engineered alkaline protease, useful particularly in laundry
PT detergents, comprising specified amino acids at particular positions.
XX
XX
PS Claim 1; SEQ ID NO 1; 31pp; English.
XX
XX The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents the wild-type Bacillus sp. KSM-KP43 alkaline
CC protease, KP43.
XX
XX Sequence 434 AA;
SQ

Query Match 99.6%; Score 2242; DB 8; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTGTVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGTVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGAYTTDSRNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARHTNSWGAANGAYTTDSRNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSGVSADNINHVAQFSRSGPTKDGRIKPDVMAPGTIFILSARSLAPDSF 240
DB 181 TVGATENLRPSGVSADNINHVAQFSRSGPTKDGRIKPDVMAPGTIFILSARSLAPDSF 240
QY 241 WANHDSKVAYMGTSMTATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAAGADIGLY 300
DB 241 WANHDSKVAYMGTSMTATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNOGWRVTLDDKSLNVAYVNESSLSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360

DB 301 PNGNOGWRVTLDDKSLNVAYVNESSLSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLDELVTAPNGTQYVGNDFTSFYNDNWDGRNNVENVFINAPQSQGYTIEVQAYN 420
DB 361 SVTLVNDLDELVTAPNGTQYVGNDFTSFYNDNWDGRNNVENVFINAPQSQGYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434
RESULT 9
ADT49604
ID ADT49604 standard; protein; 434 AA.
XX
AC ADT49604;
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease mature protein fragment.
XX
XX Alkaline protease; detergent; fiber modification; leather processing;
KW cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
XX
OS Bacillus sp. KSM-KP43.
XX
XX EPI1466970-A1.
XX
PD 13-OCT-2004.
XX
XX 08-APR-2004; 2004EP-00008605.
XX
XX 10-APR-2003; 2003JP-00106708.
XX
XX (KAOS) KAO CORP.
XX
XX Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
PI WPI; 2004-711313/70.
DR N-PSDB; ADT49605.
XX
DR New engineered alkaline protease with improved activity and thermal
PT stability, useful particularly in detergents such as laundry detergents.
XX
XX Claim 1; SEQ ID NO 1; 35pp; English.
XX
XX The invention relates to an alkaline protease and its encoding gene. The
CC alkaline protease can be expressed by standard recombinant methodology.
CC The alkaline protease is useful in the industry particularly in
CC detergents such as laundry detergents, but also in fiber modifying
CC agents, leather processing agents, cosmetic compositions, bath additives,
CC food-modifying agents, and pharmaceuticals. The enzyme has good activity
CC and thermal stability. The present sequence represents a mature alkaline
XX protease from Bacillus sp. KSM-KP43.
SQ Sequence 434 AA;
Query Match 99.6%; Score 2242; DB 8; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTGTVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGTVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGAYTTDSRNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARHTNSWGAANGAYTTDSRNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSLAPDSSF 240
 Db 181 TVGATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSLAPDSSF 240
 QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGIITPKPSLLKAALIAGAADIIGLY 300
 Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGIITPKPSLLKAALIAGAADIIGLY 300
 QY 301 PNGNOGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
 Db 301 PNGNOGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
 QY 361 SVTLVNDLDELVTAPNGTQVGNDFTSFYNDNWDGRNNVFNAPQSGTYYTIEVOAYN 420
 Db 361 SVTLVNDLDELVTAPNGTQVGNDFTSFYNDNWDGRNNVFNAPQSGTYYTIEVOAYN 420
 QY 421 VPVGPQTFSIAIVN 434
 Db 421 VPVGPQTFSIAIVN 434
 RESULT 10
 AAY17090
 ID AAY17090 standard; protein; 640 AA.
 XX AC AAY17090;
 XX DT 20-MAR-2003 (revised)
 DT 21-JUL-1999 (first entry)
 XX DE Bacillus alkaline protease.
 XX KW Alkaline protease; Bacillus; casein digestion; oleic acid; enzyme;
 KW washing composition; oxidising agent.
 XX OS Bacillus sp.
 XX PN WO9918218-Al.
 XX PD 15-APR-1999.
 PF 07-OCT-1998; 98WO-JP004528.
 XX PR 07-OCT-1997; 97JP-00274570.
 XX PA (KAOS) KAO CORP.
 XX PI Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;
 PI Shikata S, Nomura M;
 XX WPI; 1999-287736/27.
 DR N-PSDB; AAX37278.
 XX PT Alkali protease from Bacillus used in washing powders.
 XX PS Disclosure; Page 58-63; 71pp; Japanese.
 CC The invention relates to alkaline proteases produced by strains of
 CC Bacillus. The proteases ability to digest casein is not inhibited by
 CC oleic acid and they have a high stability to oxidising agents. The
 CC alkaline protease of the invention has the following properties: (a) it
 CC is active over the pH range 4-13 and has at least 80% of its optimum
 CC activity over the pH range 6-12; (b) after 30 minutes at 40 deg. C it is
 CC stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)
 CC its ability to digest casein is not inhibited by oleic acid; (e) it has
 CC molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be
 CC used as enzymes in washing compositions for use in automatic dishwashers
 CC and for washing clothes. The stability to oxidising agents allows the
 CC enzyme to be an effective component of washing compositions including
 CC bleaches. The present sequence represents an alkaline protease. (Updated
 CC on 20-MAR-2003 to correct DR field.)
 XX

SQ Sequence 640 AA;
 Query Match 99.6%; Score 2242; DB 2; Length 640;
 Best Local Similarity 99.8%; Pred. No. 2.6e-159;
 Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
 Db 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
 QY 61 NANTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSDGGLGGLPSNLQTLFQAYS 120
 Db 267 NANTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSDGGLGGLPSNLQTLFQAYS 326
 QY 121 AGARHTNSWGAANGVATTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
 Db 327 AGARHTNSWGAANGVATTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386
 QY 181 TVGATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSLAPDSSF 240
 Db 387 TVGATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSLAPDSSF 446
 QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGIITPKPSLLKAALIAGAADIIGLY 300
 Db 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGIITPKPSLLKAALIAGAADIIGLY 506
 QY 301 PNGNOGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
 Db 507 PNGNOGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 566
 QY 361 SVTLVNDLDELVTAPNGTQVGNDFTSFYNDNWDGRNNVFNAPQSGTYYTIEVOAYN 420
 Db 567 SVTLVNDLDELVTAPNGTQVGNDFTSFYNDNWDGRNNVFNAPQSGTYYTIEVOAYN 626
 QY 421 VPVGPQTFSIAIVN 434
 Db 627 VPVGPQTFSIAIVN 640
 RESULT 11
 ADM40773
 ID ADM40773 standard; protein; 640 AA.
 XX AC ADM40773;
 XX DT 01-JUL-2004 (first entry)
 XX DE Alkaline protease from Bacillus sp. KSM-KP43.
 XX KW alkaline protease; laundry detergent; bleaching agent; detergent;
 KW denture-cleaning agent; enzyme.
 XX OS Bacillus sp.; KSM-KP43.
 XX PN US2004072321-Al.
 XX PD 15-APR-2004.
 XX PF 09-JUN-2003; 2003US-00456479.
 XX PR 26-JUN-2002; 2002JP-00186387.
 XX PR 18-OCT-2002; 2002JP-00304232.
 XX PA (KAOS) KAO CORP.
 XX PI Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
 XX WPI; 2004-328572/30.
 DR N-PSDB; ADM40772.
 XX New alkaline protease having a mutant prepro sequence where amino acid
 PT residues at positions 52, 75 and 142 are substituted with another amino
 PT acid residue, useful as enzyme component of laundry detergents, or

PT bleaching agents.

PS Disclosure; SEQ ID NO 4; 29pp; English.

XX

CC The invention relates to an alkaline protease having a prepro sequence.

CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino acid residues at: (a) position 52 is substituted by aspartic acid or arginine; (b) position 75 is substituted by alanine or arginine; and (c) position 142 is substituted by lysine. The alkaline protease is useful as an enzyme which can be incorporated into laundry detergents, bleaching agents, detergents for cleaning hard surfaces or drainpipes, denture-cleaning agents, and detergents for sterilising medical apparatus. The present sequence represents alkaline protease from *Bacillus* sp. KSM-KP43.

XX Sequence 640 AA;

SEQ

Query Match 99.6%; Score 2242; DB 8; Length 640;

Best Local Similarity 99.8%; Pred. No. 2.6e-159;

Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

DB 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 266

QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120

DB 267 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

QY 181 TVGATENLRPFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240

DB 387 TVGATENLRPFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 446

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIGLY 300

DB 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIGLY 506

QY 301 PNGNCGWRVTLDKSLNVAYVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

DB 507 PNGNCGWRVTLDKSLNVAYVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566

QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGNNVNFVFINAQSGTGTITIEVQAYN 420

DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGNNVNFVFINAQSGTGTITIEVQAYN 626

QY 421 VPVGPOTFSLAVN 434

DB 627 VPVGPOTFSLAVN 640

RESULT 12

ADS14437

ID ADS14437 standard; protein; 640 AA.

XX

AC ADS14437;

XX

DT 30-DEC-2004 (first entry)

XX

DE *Bacillus* alkaline protease KP43.

XX

XX protease; enzyme; alkaline protease; laundry detergent; KP43.

XX

OS *Bacillus* sp.; KSM-KP43.

XX

XX Key Location/Qualifiers

XX

XX Key 1..206

XX

XX Peptide 207..640

XX

XX Protein

XX

XX

XX

PN EP1466962-A1.

XX 13-OCT-2004.

XX

XX 08-APR-2004; 2004EP-00008604.

XX

XX 10-APR-2003; 2003JP-00106709.

XX

XX (KAOS) KAO CORP.

XX

PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;

XX

XX WPI; 2004-711313/70.

DR N-P8DB; ADS14428.

XX

XX New engineered alkaline protease, useful particularly in laundry

PT detergents, comprising specified amino acids at particular positions.

PT

XX Disclosure; SEQ ID NO 1; 31pp; English.

XX

XX The invention relates to a novel alkaline protease. The new alkaline protease comprises an amino acid sequence in which one or more amino acid residues selected from those located at 7 specific positions within ADS14427, or at positions corresponding to these positions are: position 15 (histidine), position 16 (threonine or glutamine), position 166 (glycine), position 167 (valine), position 187 (serine), position 346 (arginine), and position 405 (aspartic acid). The alkaline protease is useful in industry particularly in laundry detergents, but also e.g. in fibre modifying agents, leather processing agents, cosmetic compositions, bath additives, food-modifying agents, and pharmaceuticals. The present sequence represents the wild-type *Bacillus* sp. KSM-KP43 alkaline protease, KP43. The sequence is shown in the sequence listing as part of SEQ ID NO:1

XX

XX Sequence 640 AA;

SEQ

Query Match 99.6%; Score 2242; DB 8; Length 640;

Best Local Similarity 99.8%; Pred. No. 2.6e-159;

Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

DB 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 266

QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120

DB 267 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

QY 181 TVGATENLRPFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240

DB 387 TVGATENLRPFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 446

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIGLY 300

DB 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIGLY 506

QY 301 PNGNCGWRVTLDKSLNVAYVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

DB 507 PNGNCGWRVTLDKSLNVAYVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566

QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGNNVNFVFINAQSGTGTITIEVQAYN 420

DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGNNVNFVFINAQSGTGTITIEVQAYN 626

QY 421 VPVGPOTFSLAVN 434

DB 627 VPVGPOTFSLAVN 640

RESULT 13

ADT49613
ID ADT49613 standard; protein; 641 AA.
XX
AC ADT49613;
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease.
XX
KW Alkaline protease; detergent; fiber modification; leather processing;
KW cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
XX
OS Bacillus sp. KSM-KP43.
XX
FH Key Location/Qualifiers
FT Peptide 1..206
FT /note= "signal peptide"
FT Protein 207..641
FT /note= "specifically claimed mature protein (SEQ ID 1)"
XX
PN EPI466970-A1.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008605.
XX
PR 10-APR-2003; 2003JP-00106708.
XX
PA (KAOS) KAO CORP.
XX
PI Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
XX WPI; 2004-711317/70.
DR N-PSDB; ADT49605.
XX
PT New engineered alkaline protease with improved activity and thermal
PT stability, useful particularly in detergents such as laundry detergents.
PS Disclosure; Page 19-25; 35pp; English.
XX
CC The invention relates to an alkaline protease and its encoding gene. The
CC alkaline protease can be expressed by standard recombinant methodology.
CC The alkaline protease is useful in the industry particularly in
CC detergents such as laundry detergents, but also in fiber modifying
CC agents, leather processing agents, cosmetic compositions, bath additives,
CC food-modifying agents, and pharmaceuticals. The enzyme has good activity
CC and thermal stability. The present sequence represents an alkaline
CC protease from Bacillus sp. KSM-KP43.

Sequence 641 AA;
Query Match 99.6%; Score 2242; DB 8; Length 641;
Best Local Similarity 99.8%; Pred. No. 2.6e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQAHSYGLYGQGQIVAVADTGTDGRNDSMHEAFRGKITAYALGRTN 60
Db 207 NDVARGIVKADVAQAHSYGLYGQGQIVAVADTGTDGRNDSMHEAFRGKITAYALGRTN 266

Qy 61 NANDTNHGTHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTILFSQAYS 120
Db 267 NANDTNHGTHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTILFSQAYS 326

Qy 121 AGARIHTNSGWAVNCAYTTDSRNVDVVYRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180
Db 327 AGARIHTNSGWAVNCAYTTDSRNVDVVYRKNDMTILFAAGNEGPGGTISAPGTAKNAI 386

Qy 181 TVGATENLPSPFGSYADNNHVAQFSRRGPKDVPMAQPTFILSARSSLPDSSF 240
Db 387 TVGATENLPSPFGSYADNNHVAQFSRRGPKDVPMAQPTFILSARSSLPDSSF 446

Qy 241 WANHDSKYAMCGTSMATPIVAGNVAQLREHFVKVRGITTPKPSLLKAAIIAGAADIIGLY 300

CC information given in Example 1.

XX Sequence 434 AA;

Query Match 99.5%; Score 2239; DB 8; Length 434;
Best Local Similarity 99.3%; Pred. No. 2.6e-159;
Matches 431; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGTGVAGSVLGNSTKMGAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGVAGSVLGNSTKMGAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARIHTNSWGAANGAYTTDSRNVDVYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGAYTTDSRNVDVYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKDVMAPGTFILSARSLAPDSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKDVMAPGTFILSARSLAPDSF 240

QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300

QY 301 PNGNGQWGRVTLDKSLNVAIYVNESSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNGQWGRVTLDKSLNVAIYVNESSLSTSQKATYSFTATAGKPLRISLVWSDAPASTTA 360

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSFYNDWGRNNVNFVINAPOSQGTYYTIEVQAYN 420
DB 361 SVTLVNDLDLVTAPNGTQYVGNDFTSFYNDWGRNNVNFVINAPOSQGTYYTIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 15

ADM40780

ID ADM40780 standard; protein; 434 AA.

XX AC ADM40780;

XX 01-JUL-2004 (first entry)

XX Alkaline protease #2 from Bacillus sp. KSM-KP9865.

XX alkaline protease; laundry detergent; bleaching agent; detergent;

XX denture-cleaning agent; enzyme.

XX Bacillus sp.; KSM-KP9865.

XX US2004072321-A1.

XX 15-APR-2004.

XX 09-JUN-2003; 2003US-00456479.

XX 26-JUN-2002; 2002JP-00186387.

XX 18-OCT-2002; 2002JP-00304232.

XX (KAOS) KAO CORP.

XX Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;

XX WPI; 2004-328572/30.

XX New alkaline protease having a mutant prepro sequence where amino acid

XX residues at positions 52, 75 and 142 are substituted with another amino

XX PT

PT acid residue, useful as enzyme component of laundry detergents, or
XX bleaching agents.

PS Disclosure; SEQ ID NO 11; 29pp; English.

XX The invention relates to an alkaline protease having a prepro sequence.
CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
CC acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
CC acid residues at: (a) position 52 is substituted by aspartic acid or
CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
CC position 142 is substituted by lysine. The alkaline protease is useful as
CC an enzyme which can be incorporated into laundry detergents, bleaching
CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
CC cleaning agents, and detergents for sterilising medical apparatus. The
CC present sequence represents an alkaline protease used in homology
CC comparison with alkaline protease from Bacillus sp. KSM-KP43.

XX Sequence 434 AA;

Query Match 99.4%; Score 2237; DB 8; Length 434;
Best Local Similarity 99.5%; Pred. No. 3.6e-159;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGTGVAGSVLGNSTKMGAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGVAGSVLGNSTKMGAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARIHTNSWGAANGAYTTDSRNVDVYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGAYTTDSRNVDVYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKDVMAPGTFILSARSLAPDSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKDVMAPGTFILSARSLAPDSF 240

QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300

QY 301 PNGNGQWGRVTLDKSLNVAIYVNESSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNGQWGRVTLDKSLNVAIYVNESSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSFYNDWGRNNVNFVINAPOSQGTYYTIEVQAYN 420
DB 361 SVTLVNDLDLVTAPNGTQYVGNDFTSFYNDWGRNNVNFVINAPOSQGTYYTIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

Search completed: April 7, 2006, 09:29:28

Job time : 95 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:32:05 ; Search time 25 Seconds
(without alignments)
1670.323 Million cell updates/sec

Title: US-10-820-714A-1-HIS15
Perfect score: 2251
Sequence: 1 NDVARGIVKADVAQHSYGLY.....EVOQAVNPVGQTFSLAIVN 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: Pirl: *
2: Pirl2: *
3: Pirl3: *
4: Pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	523.5	23.3	1743	2	T18279
2	497	22.1	1905	2	T18267
3	347.5	15.4	444	2	B83891
4	320.5	14.2	442	2	A69587
5	310.5	13.8	806	2	A41341
6	302.5	13.4	1398	2	T28159
7	283	12.6	580	2	S11890
8	281	12.5	419	1	S25835
9	280	12.4	799	2	G83753
10	279.5	12.4	1345	2	T29090
11	277	12.3	420	1	S23407
12	267	11.9	715	2	JC4908
13	261	11.6	1331	1	A72647
14	259.5	11.5	513	1	A35742
15	259.5	11.5	757	2	C84120
16	253.5	11.3	894	2	F69730
17	251	11.2	627	2	D75393
18	248.5	11.0	380	2	A49778
19	246.5	11.0	402	1	JU0332
20	246.5	11.0	534	1	JS0173
21	244.5	10.9	382	1	SUBSN
22	242.5	10.8	519	2	S71451
23	241.5	10.7	401	2	I35974
24	240	10.7	488	2	A11930
25	235	10.4	382	2	JH0778
26	234.5	10.4	381	2	A33973
27	234	10.4	378	2	A33973
28	234	10.4	910	2	C69456
29	234	10.4	1374	2	D72593

30	232.5	10.3	381	1	SUBSI	subtilisin (EC 3.4
31	232.5	10.3	381	1	SUBSS	subtilisin (EC 3.4
32	232.5	10.3	381	2	JQ1487	subtilisin (EC 3.4
33	232.5	10.3	525	2	G84406	halolysin (impor
34	231	10.3	321	1	S27501	alkaline protein
35	230.5	10.2	272	2	A23624	subtilisin (EC 3.4
36	229.5	10.2	379	1	SUBSCL	subtilisin (EC 3.4
37	229.5	10.2	601	2	JC4576	serine proteinase
38	227	10.1	1167	1	A35066	streptococcal C5a
39	226.5	10.1	1118	2	H97298	subtilisin like pr
40	225.5	10.0	1052	2	T17093	intraluminal subti
41	224	10.0	613	2	S75976	hypothetical prote
42	223.5	9.9	361	2	A48373	high-alkaline seri
43	221.5	9.8	275	2	JC1085	subtilisin (EC 3.4
44	221.5	9.8	261	2	G83756	subtilisin-type al
45	221.5	9.8	530	2	A42605	halolysin (EC 3.4

ALIGNMENTS

RESULT 1

T18279
multidrug resistance transport protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18279
R:Shaulsky, G.; Loomis, W.F.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z18855
A:Accession: T18279
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1743 <SHA>
A:Cross-references: UNIPROT:Q23868; UNIPARC:UPI000013687D; EMBL:U60086; NID:gl1399914; PII

Query Match 23.3%; Score 523.5; DB 2; Length 1743;
Best Local Similarity 27.9%; Pred. No. 2.9e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

QY 19 LVGQGIIVAVADTGLDTGR---NDS-----SMHEAPRGKITALYALGRTNNDTNGH 68
DB 314 LRKGQILSIADTGLDGHCFPSDSKYPIPLNSVLNHR-KVVTYITTSDDSKVDGH 372
QY 69 GTHVAGSVLG-----NGSTNKGMAPQANLVFQSIMDSGGGLGGL--PSNLTQLFSQAY 119
DB 373 GTHICGSAAGTPEDSSVNISSFGSLATDAKIAF---FDLASGSSSLTPFSDLKQLYQPLY 429
QY 120 SAGARIHNSWGA----AVNGAYTTDSRNVDDYVRKN-DMTILFAAGNPGNGGTIS--A 172
DB 430 DAGARVHCDSWGVSVEGTGYSSSDTASIDFLFTHPDFFILRAAGN---NEQVLSLIT 486
QY 173 PCTAKNAITVGATENLR-----PSFGSYADNI-----PSFGSYADNI----- 199
DB 487 OSTAKNVITVGAHQTHENYLTGDNINYSQSDVINQBELICDFDSRYCNYTTAQCLSES 546
QY 200 -----NHVAQFSRSGPTKDGRIKPDVMAQGTFL 228
DB 547 NATTGLASCCPTLLRKSVIDAANTQPLLNNENNICSFSKSGPTHGDMKPAVAPGEYIT 606
QY 229 SARSSLA-----PSSSWANHDSKYVYGGTSMATPIVAGNVAQLREH-----F 272
DB 607 SARSGANTTDCQDGSIL-PNTNALLA-ISGTSMATSFAAAAATTLRLQYLVDDGYPTGSI 664
QY 273 VKNRGITPKPSLLKAALTAGA-----ADIGLYPENG-----ADIGLYPENG----- 311
DB 665 VESNKLQPTGSLKALMINNAQLNGTQLTSSSTYPSNVFENFAGASLVQGWGAIR 724
QY 312 LDKSLNVAYNVNESS-----ADIGLYPENG-----ADIGLYPENG----- 338
DB 725 MSNWLHVNNNSNNNNKTSDCITKFDGIGGLDLRLVKPNQWKEESLSTGQNTSYCTYK 784

A:Authors: 1-442 <KUN>
A:Cross-references: UNIPROT:O31788; UNIPARC:UPI000006043P; GB:Z99113; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
F:146-398/Domain: subtilisin homology <SBT>
Query Match 14.2%; Score 320.5; DB 2; Length 442;
Best Local Similarity 29.7%; Pred. No. 3.9e-13;
Matches 107; Conservative 50; Mismatches 104; Indels 99; Gaps 16;
QY 11 DVAQHSYGLYGQCOQIVAVADTGLDTRNDSDMHEAPRGKITALYALGRNNAN-----D 64
DB 136 EVVRNGQTLTGKVTAVVDTGI-----YHPDLEGR-----IGFADVMVNQKTEPYD 183
QY 65 TNGHGHVAGSVLNGSTN-----KGMAPQANLVFQSDMSSGGGLGGLPSNLQTLFQSAYS 120
DB 184 DNGHGHVAGSVLNGSTN-----KGMAPQANLVFQSDMSSGGGLGGLPSNLQTLFQSAYS 120
QY 121 AGARIHTNSWGAIVN-----GAYTDSRNVDYVYKND-----MTIL 157
DB 237 -----EMCTQYNEDNPEIDIMMSGLGDALRYDHEQDPLVRAVEEAWAGIVVC 288
QY 158 FAAGNEGNGGTTASPTAKNAITVGCATENLRPSFGSYADNINHVAQFSRGTGDKGRITK 217
DB 289 VAAGNSGPPQSTIASPGVSEKVIITVGLADNNTA-----SSDDTVAASFSSRGTPTVYGREK 344
QY 218 PDVMAPGTPTILSARSLAPDSSP-----WANHDSKYAVMGGTSMTPTPIVAGNVAQLREHF 272
DB 345 PDILAPGVNIIISLR-----PNSYIDKLQKSRVSGSYFTWSTGTSMTPTPIVAGNVAQLREHF 272
QY 273 VKNRGITPK--PELLKAAIAGAADIGLYPNGNQGWRTLDKSLNV---AYVNESSL 327
DB 400 -QNPDLTPDEVKELLK-----NGTDKW-----KDEDPNIIYGAGVNAENSV 439
RESULT 5
A41341
Microbial serine proteinase (BC 3.4.21.-), minor (vpr), precursor - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
A:Accession: A41341; B41341; S39730; D69730
R:Sloma, A.; Rufo Jr., G.A.; Theriault, K.A.; Dwyer, M.; Wilson, S.W.; Pero, J.
J. Bacteriol. 173, 6889-6895, 1991
A:Title: Cloning and characterization of the gene for an additional extracellular serine
A:Reference number: A41341; MUID:92041574; PMID:1938892
A:Accession: A41341
A:Molecule type: DNA
A:Residues: 1-806 <SLO>
A:Cross-references: UNIPROT:P29141; UNIPARC:UPI0000060C20; GB:M76590; NID:G143819; PIDN:
A:Accession: B41341
A:Molecule type: protein
A:Residues: 161-195 <SL2>
A:Cross-references: UNIPARC:UPI0000178D67
R:Glaser, P.; Kunst, F.; Arnaut, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu,
A.; Rapoport, G.; Danchin, A.
Mol. Microbiol. 10, 371-384, 1993
A:Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr
A:Reference number: S39655; MUID:95020537; PMID:7934828
A:Accession: S39700
A:Molecule type: DNA
A:Residues: 1-806 <GLA>
A:Cross-references: UNIPARC:UPI0000060C20; EMBL:X73124; NID:G413923; PIDN:CAAS1601.1; PI
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, N.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eirington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Mausel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosa, V.; Uchiyama,
I.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69730
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-806 <KUN>
A:Cross-references: UNIPARC:UPI0000060C20; GB:Z99123; GB:AL009126; NID:G2636240; PIDN:CAI
A:Experimental source: strain 168
C:Comment: The amino terminal sequence of the mature protein and a molecular weight of or
C:Genetics:
A:Gene: vpr
A:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-160/Domain: propeptide #status predicted <PRO>
F:180-548/Domain: subtilisin homology #status atypical <SBT>
Query Match 13.8%; Score 310.5; DB 2; Length 806;
Best Local Similarity 23.5%; Pred. No. 3.8e-12;
Matches 129; Conservative 58; Mismatches 157; Indels 205; Gaps 18;
QY 18 GLYGGQIVAVADTGLDTGR-----NDSSMHEAPRGKITALYALGRTN 60
DB 177 GVTGKGIKVAIIDTGVYNNHPLKKNFGQYKGVDFVNDYDPKETPTG-----D 225
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSDMSSGGGLGGLPSNLQTLFQSAYS 120
DB 226 PRGEATDGHGHVAGTVAANG--TIKGVAPDATTLLAVRVLPGFG--SETTENVIAGVBRVQ 282
QY 121 AGARIHTNSWGAIVN-----GAYTDSRNVDYVYKNDMTILFAAGNEGNGGTTASPTAKNAI 180
DB 283 DGADVMNLSLNGSLNPNPWATSTAL--DWAMSEGVAVTSGNSGPNGTWVSGPTSRGAI 341
QY 181 TVGATE-----NURPSFGSY-----195
DB 342 SVGATQLPLNEYAVTFGYSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKDFEGKDLT 401
QY 196 -----ADNI-----199
DB 402 GKAVVYKRSIAFVDKADNAKAGAGMVMVNNLSGEIEANVPMSVPTIKLSLEGEKL 461
QY 200 -----NHVAQFSRGTPTK--GRIPKPDVMAPTGTFILSARSLAP 236
DB 462 VSALKAGETKTFTKLTIVSKALGEQVADFSRSGPVMVTWIKPDISAPGVNIVSTIPTHDP 521
QY 237 DSSFVWANDSKYAVMGGTSMTPTPIVAGNVAQLREHFVKNRGITPKPSL--LKAALIAGAA 294
DB 522 D-----HPYGYGSKQGTSMASPHIAGAVAVIKQ-----AKPKWSVEQIKAAIMNTAV 568
QY 295 DI-----GLGYPNGNQGWRTLDKSLNVAYVNESSLTSQKATYSFTATAGKPLKISLV 350
DB 569 TLKDSDDGEYYPHNAQAGSARI-----MNAIKADSLVSPGYSY-----GTFLK---- 612
QY 351 WSDAPASTTASTVANDLDELVTAPNGTOYVGNDFSPYNDNDWG--RNNVENVFVINAQ 408
DB 613 -ENGNETKNETFTIENQ-----SSIRKSTILEYSPNGSGISTSGTSRVRVIPAQ 660
QY 409 SGTYTIEVQ 417
DB 661 TCKATAKVK 669
RESULT 6
T28159
pyrolysin (EC 3.4.-.-) - Pyrococcus furiosus
C:Species: Pyrococcus furiosus
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28159

R:Voorthorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, R.J.; Vos, J. Biol. Chem. 271, 20426-20431, 1996
A:Title: Isolation and characterization of the hyperthermostable serine protease, pyroly
A:Reference number: Z20481; MUID:96355370; PMID:8702780

A:Accession: T28159
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1398 <VOO>
A:Cross-references: UNIPROT:P72186; UNIPARC:UPI000016FD59; EMBL:U55835; NID:g1556462; PI
A:Experimental source: DSN3638
C:Genetics:
C:Gene: pls
C:Keywords: hydrolase; serine proteinase

Query Match 13.4%; Score 302.5; DB 2; Length 1398;
Best Local Similarity 26.6%; Pred. No. 2.6e-11;
Matches 139; Conservative 57; Mismatches 178; Indels 149; Gaps 22;
QY 21 GOGQIVAVADTGLDGRNDS-----SMHEAFRGKITALYALGRTNAN----- 63
DB 301 GNGYDIAYVDTLDYDFTDEVLPGQYNYVDYVAVFSYVYVPLNYVLAEDPGEYAVFCW 360
QY 64 DTNGHGHVAGSVLNGSTN-----KGMAPQAN 91
DB 361 DGHGHGHVAGTVAGYDSNDAWDLMSYSGEWEVFSRLYGYWDTYNTVTDTVQGVAPGAQ 420
QY 92 LVFQSIMSGGLGLPSNLQTLFSQAYSAGARIHTNSWGAANGAYT--TDSRN--VDD 147
DB 421 INAIRVLR--DGRGSMWDIIEGM--TYAATHGADVISMISLGG--NAPYLDGTDPSVAVDE 476
QY 148 YVRKNDMTILFAAGNEGPNNGTISAPGTAKNAITVGATENLRPSFGSYAD----- 197
DB 477 LTEKGVVFPVIAAGNEGGINVSGVATKAITVGAAA--VPINGVVYSQALGYPDYVG 535
QY 198 -----NINHVAQFSSRGPTKGRIPKPDVNPAGTIFILSARSLAPDSSFWANHDSKYA 249
DB 536 FYYFPAYTNV--RIAFSSRGPRIDGEIKDNVAVPGYVIGYVSLPMWIGGADF----- 585
QY 250 YNGGTSMTPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADI-----GLYPNG 303
DB 586 -MSGTSMTAPHPVGVALLISG--PKPEGIYVNPDIKKVLESGATWLEGDPVTGOKYTEL 643
QY 304 NGGWRVTLDKSLNVAYNNESSLSSTSKATYSFTATAGTKPLKISLVMSDAPASTTA--- 360
DB 644 DQGHGLNVNKSWEI-----LKAINGTTLPIVDHWADKYSDFAEYL 685
QY 361 SVTLVNDLVLITAPN-----GTQYVGN-----DFTSPYNDW-----DG-----RNNVNVF 403
DB 686 GVDVIRGLYARNSIPDIVEMHKKYVGDTEYRTEFYATEPWIKPFVSGSVILENNTEFVL 745
QY 404 -----INAPQSGTY-----TIEVQAYNVVPGPQTF 429
DB 746 RVKYDVEGLEPLGLYGRRIIDPTFTVIBDEILNTVIVPEKFT 788

RESULT 7
S11890
serine proteinase (EC 3.4.21.-) precursor, extracellular - Xanthomonas campestris pv. ca
N:Alternate names: subtilisin-related proteinase
C:Species: Xanthomonas campestris pv. campestris
C:Date: 21-Nov-1993 #sequence_revision 07-Feb-1997 #text_change 31-Dec-2004
A:Accession: S11890
R:Jiu, Y.N.; Tang, J.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J.
Mol. Gen. Genet. 220, 433-440, 1990
A:Title: A multipurpose broad host range cloning vector and its use to characterise an e
A:Reference number: S11890; MUID:90251253; PMID:2187155
A:Molecule type: DNA
A:Residues: 1-580 <LIU>
A:Cross-references: UNIPROT:P23314; UNIPARC:UPI000012A398; EMBL:X51635; NID:g48533; PIDN
A:Experimental source: Xanthomonas campestris pv. campestris
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 3 in having 205-Ala
C:Superfamily: extracellular alkaline serine protease precursor, Alteromonas type

C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:168-423/Domain: subtilisin homology <SBT>

Query Match 12.6%; Score 283; DB 2; Length 580;
Best Local Similarity 26.2%; Pred. No. 1.4e-10;
Matches 127; Conservative 55; Mismatches 147; Indels 156; Gaps 24;
QY 21 GOGQIVAVADTGL-----DTGRNDSMHEAFRGKITALYALGRTNAND----- 64
DB 168 GSGTVVAVIDGITSHADLNANILAGYDFISDAITARDGNGRDSNAADGDGHWAAECCA 227

QY 65 -----TNGHGHVAGSVLNGSTNKGMAPQ-----NLVFSQIMD 99
DB 228 GIPAASSSMHGHVAGTVAAVTNNTTGVAGTAYGAKVVPVRVLGKCGGSLSDIADAIVWA 287
QY 100 SGGGLGLPSNLQ--TLFSQAYSAGARIHTNSWGAANGAYT--TDSRNVDVYVRKNDMTIL 157
DB 288 SGGTVSGIPANANPAEIVNMSLGGGSCSTTQON--AINGAVSRGT-----TVV 334
QY 158 FAAGNEGPNNGTISAPGTAKNAITVGATEN--LRPSFGSYADNINHVAQFSSRGPTKQGR 215
DB 335 VAAGNDANVSG--SLPANCANVIAVAATTSAGAKASYNPGTGI----- 377
QY 216 IKPDVNPAGTIFILSARSS--LAPDSSFWANHDSKYAYMGTSMTPIVAGNVAQLREHPV 273
DB 378 ---DVSAPGSSILSTLNSGTTTPGS-----ASYANGTSMAGPHVAGVALVQS--V 425
QY 274 KNRGTPK--PSLLK--AALTAGADIGLVPNGQGRVTLDKSLNVAYNNESS----- 325
DB 426 APTALTPAAVETLLKNTARALPGAC-----SGCGGAGIVNADAATAVTA--INGSGGGG 477
QY 326 -----SLTSOKATYSFTATAGTKPLKISLVMSDAPASTTASVTL--VND 367
DB 478 GGNLTNGTNPVTGLGAATGAELNITITVPAG-----SGTLVTTSGGSD 523
QY 368 LDLVI---TAPNGTOYVGNDEFTSPYNDNWDGRRNNVNFVINAQSGTGYTIEVQAYNVPG 424
DB 524 ADLYVRAGSAPDTSAYT---CRPYRS-----GNAETCTITAP--SGTYVVRLKAYS----- 569
QY 425 POTFS 429
DB 570 --TFS 572

RESULT 8
S25835
subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41)
C:Species: Bacillus sp.
C:Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
A:Accession: S25835
R:Davail, S.; Feller, G.; Narinx, E.; Gerday, C.
Gene 119, 143-144, 1992
A:Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacillus
A:Reference number: S25835; MUID:93012966; PMID:1398082
A:Accession: S25835
A:Molecule type: DNA
A:Residues: 1-419 <DAV>
A:Cross-references: UNIPARC:UPI00000BB77A; EMBL:X63533; NID:g40198; PIDN:CAA45096.1; PID:
C:Superfamily: Subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-110/Domain: propeptide #status predicted <PRO>
F:111-419/Product: microbial serine proteinase #status predicted <MAT>
F:135-373/Domain: subtilisin homology <SBT>
F:144,184,359/Active site: Asp, His, Ser #status predicted

Query Match 12.5%; Score 281; DB 1; Length 419;
Best Local Similarity 33.0%; Pred. No. 1.2e-10;
Matches 87; Conservative 38; Mismatches 97; Indels 42; Gaps 13;
QY 21 GOGQIVAVADTGLDGRNDSMMH--BAFRGKITALYALGR-----NNANDTNGHGHVAGSV 76

Db 135 GAGINAVLDTGVNTWHPDLSNNVEQKD-----FTVGTNFTDNSCTDRQGHGTHVAGSA 189
Qy 77 LGNGSTNK---GMAPQANL-VFQSIMDSGGGLG-GLPSNLQTLFQSAQYAGARIHTN-SW 130
Db 190 LANGGTGSGVYGVYGAPEADLWAYKVLGDDGSGYADDIAEAIRHAGDQATALTAKVINMSL 249
Qy 131 GAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAITVGATENLRP 190
Db 250 GSGGESSLIT---NAVYAYDKGLVLLIAAGNSGPKPGSIGYPGALUNAVAALENTIQ 306
Qy 191 SFGSYADNINHVAQFSRSGPTKDG-----RIKPDVMAFGTFTLSARSSLAPDSSFWANH 244
Db 307 N-GTY-----RVADFSSRGHKRTAGDYVIQKGDVEISAPGAAYYST-----W-P 348
Qy 245 DSKYAYMGTSMTATPIVAGNAQL 268
Db 349 DGGYATISGTSNASPHAAGLAARI 372

RESULT 9
G83753
subtilisin-type proteinase (EC 3.4.21.-) vpr precursor [similarity] - Bacillus haloduran
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83753
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-799 <STO>
A:Cross-references: UNIPROT:Q9KEM1; UNIPARC:UPI00000C39DC; GB:AP001510; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: vpr
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-29/Domain: signal sequence #status predicted <SIG>

Query Match 12.4%; Score 280; DB 2; Length 799;
Best Local Similarity 24.7%; Pred. No. 3.3e-10;
Matches 117; Conservative 50; Mismatches 135; Indels 172; Gaps 16;
Qy 18 GLYGQGIIVAVADTGLDTRGNDSSMHEAFRGKITALYALGRTNANDT-----NGH 68
Db 171 GYTGEITVAILTGVDTYTHPD--LVHAF-GDYKGWDFDNDNDPQETPPGDPGRGIEITH 227
Qy 69 GTHVAGSVLGNGSTNGKMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQSAQYAGARIHTN 128
Db 228 GTHVAGTVAANGLI-KGVAPDANLLAYRVLGPGG--RGSTAGVIAGIERAVQDGADIMNL 284
Qy 129 SNGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAITVGATENL 188
Db 285 SLGNTLNDPDFATSTIAL-DWMAEGVAVTISNGSGFNWTVGSPGTSRDAISVGAT---- 340
Qy 189 RPSFGSY-----ADNINH----- 201
Db 341 RLPYNYKASVTSDDIGDYADIMGFPSPDEILLELDGETYEYAFAGLKPQDGEVDVE 400
Qy 202 ----- 201
Db 401 GKIALIVRGEIPFVEKAENAKAAGAVGAIYNNVAGVQPTVPGLAIPITIMLSNEDGLKMR 460
Qy 202 -----VAQFSRGPT-KDGRIKPDVMAPGTFTLSARSLAPD 237
Db 461 NELENGQNTVTSIEPDKLVGETVADFSSRGPPVMTWMIKPDVSAAPVAIVSTIPTHQPD 520
Qy 238 SSGFWANHDSKYAYMGTSMTATPIVAGNAQLREHFVKNRGITPKPSLLKAAIAGAADI- 296
Db 521 DPF-----GYSGRQGTSMASPHVAGAAALLLEAH-PWGV-----DHVKAALMNTAENLV 569

Qy 297 ---GLGYPNGNOGWRVTLDKSLNAVYVNESSLSLTSQKATY-SFTATAGKPLK 346
Db 570 DENGRIYPHNTQAG-----SIRIVDAIESETLVTPGSHSFGFTFKERKQVE 617

RESULT 10
T29090
surface layer-associated STABLE proteinase - Staphylothermus marinus
N:Alternate names: hyperthermostable proteinase
C:Species: Staphylothermus marinus
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T29090
R:Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.
Curr. Biol. 6, 739-749, 1996
A:Title: A hyperthermostable protease of the subtilisin family bound to the surface layer
A:Reference number: Z20559; MUID:96385442; PMID:8793300
A:Accession: T29090
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1345 <MAY>
A:Cross-references: UNIPROT:Q54437; UNIPARC:UPI0000062778; EMBL:U57968; NID:gl374755; PII
A:Experimental source: strain F1
C:Function:
A:Description: probably serves an exodigestive function related to the organism's energy
A:Note: stoichiometric S-layer component

Query Match 12.4%; Score 279.5; DB 2; Length 1345;
Best Local Similarity 29.9%; Pred. No. 7.2e-10;
Matches 99; Conservative 45; Mismatches 106; Indels 81; Gaps 14;
Qy 46 FRGKITALVALGRNTNANDTNGHGHVA-----GSVL-----GNGSTNK-GMAPQANLV 93
Db 445 YQGRVYAL-----VSDFHGHTGSVATVIASRGRLVLDYLDGKLYRIMGVAPGAKI- 495
Qy 94 FQSIMDSGGGLGGLPSNLQTLFQSAQYAG-----EAWLAGFNIVTEEDGVVYLSLDPFGPHRAIISNSW 546
Db 496 -----AGGDWLLGNILVL--EAWLAGFNIVTEEDGVVYLSLDPFGPHRAIISNSW 546
Qy 131 GAAVNGAYTTDSRNVD-----DYVRKNDMTILFAAGNEGPNGGTISAPGTAK 177
Db 547 GSIYINFMLQPPGIDYRSSFMDEILAIRNYLIGDHVTIVFAAGNEGPGYSSNGAPGTGL 606
Qy 178 NAITVGATE-NLRPSFG---SYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFTLSARS 232
Db 607 LVITAGASTLMDYTRIYGYPEGYAD---EVIFFSRGPTGGYKPKPDIVNIGAFEWASTR 663
Qy 233 SLAPDSSFWANHDSKYAYMGTSMTATPIVAGNAQLREHFVKNRGITPKPSLLKAAIAG 292
Db 664 TI-DGRGYCAQPD---VFGGTSEATPYTSGTLALVFQAYKEVYNTTPDPVTAKIILKSS 718
Qy 293 AADIGLYPNQNGWRVTLDKSLNAVYVNE 323
Db 719 AKDI--WYPAFQSGSRVDKALKAAATVFISE 747

RESULT 11
S23407
subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39)
C:Species: Bacillus sp.
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004
C:Accession: S23407
R:Narinx, R.; Davall, S.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1131, 111-113, 1992
A:Title: Nucleotide and derived amino acid sequence of the subtilisin from the antarctic
A:Reference number: S23407; MUID:92256481; PMID:1581352
A:Accession: S23407
A:Molecule type: DNA
A:Residues: 1-420 <NAR>
A:Cross-references: UNIPROT:P28842; UNIPARC:UPI0000136183; EMBL:XG2369; NID:g40200; PIDN:
C:Genetics:
A:Gene: subtil
C:Superfamily: Subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase

Db 739 STSYENVYSLLS-----GYSYPLAPNPVEDTQIYPGVLKPGETAETLVLTKL 788

RESULT 14

A35742

aqualysin (EC 3.4.21.-) I precursor - Thermus aquaticus

C/Species: Thermus aquaticus

C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 05-Oct-2004

C/Accession: A35742; S00620; S00324

R:Terada, I.; Kwon, S.T.; Miyata, Y.; Matsuzawa, H.; Ohta, T.

J. Biol. Chem. 265, 6576-6581, 1990

A/Title: Unique precursor structure of an extracellular protease, aqualysin I, with NH-2

A/Reference number: A35742; MUID:90216674; PMID:2182621

A/Accession: A35742

A/Molecule type: DNA

A/Residues: 1-513 <TER>

A/Cross-references: UNIPROT:P08594; UNIPARC:UPI0000125D08; GB:J90108; GB:D90108; GB:J0544

A/Note: the authors translated the codon CTG for residue 470 as Val, and GGT for residue

R:Kwon, S.T.; Terada, I.; Matsuzawa, H.; Ohta, T.

Eur. J. Biochem. 173, 491-497, 1988

A/Title: Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline serine

A/Reference number: S00620; MUID:88255062; PMID:3286255

A/Accession: S00620

A/Molecule type: DNA

A/Residues: 75-442 <KWO>

A/Cross-references: UNIPARC:UPI0000170448; EMBL:X07734; NID:G48069; PIDN:CAA30559.1; PID

A/Note: part of this sequence, including the amino and carboxyl ends of the mature prote

R:Matsuzawa, H.; Tokugawa, K.; Hanaoka, M.; Mizoguchi, M.; Taguchi, H.; Terada, I.; Kwon

Eur. J. Biochem. 171, 441-447, 1988

A/Title: Purification and characterization of aqualysin I (a thermophilic alkaline serin

A/Reference number: S00324; MUID:88151937; PMID:3162211

A/Accession: S00324

A/Molecule type: protein

A/Residues: 128-170 <MAT>

A/Cross-references: UNIPARC:UPI0000172C23

C/Superfamily: Subtilisin; subtilisin homology

C/Keywords: extracellular protein; hydrolase; serine proteinase

F/1-14/Domain: signal sequence #status predicted <SIG>

F/15-127/Domain: propeptide #status predicted <PRO>

F/128-408/Product: aqualysin I #status experimental <MAT>

F/137-364/Domain: subtilisin homology <SBT>

F/255-257,281-283/Region: SI specificity crevice #status predicted

F/409-513/Domain: carboxyl-terminal propeptide #status predicted <CPR>

F/166,197,349/Active site: Asp, His, Ser #status predicted

Query Match 11.5%; Score 259.5; DB 1; Length 513;

Best Local Similarity 25.9%; Pred. No. 3.7e-09;

Matches 117; Conservative 45; Mismatches 144; Indels 145; Gaps 23;

QY 15 HSYGLYGGQGVAVADTGLDTRNDSSMHEAFRGKITALY-ALGRNTNANDTNGHGHVA 73

Db 151 YTTATGRGVNVVVDIGRT-----THREFGRARVGVYDALG--GNQDCNNGHGHVA 202

QY 74 GSYLVNGSTNKGMAPQANLVFQSIMD--SGGGLGLPLSNLQTLFQAYSAGARIHTN--- 128

Db 203 GTI---GGVTYGVAKAVNLVAVRVLDCNGSGSTSGVIAGVDMV-----TNRHRRPAV 251

QY 129 ---SWGAAVNGAYTTDSRNVDDYVRKN---DMTLFAAGNEGNGGTISAPGTAKNAIVT 182

Db 252 ANMSLGGGVSTA-----LDNVAQKSIAGVVVYVAAGNDNANACNYS-PARVAEALTV 303

QY 183 GAT--ENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTILSARSLAPDSF 240

Db 304 GATTSSDARASFNYGSCV-----DLFAPGASIPSA----- 334

QY 241 WANHDSKYATMGGTSMATPTVAGNVNAQLRHFVKNRGITP---KPSLLKAALTAGAADIG 297

Db 335 WYTSDDTATQTLNGTSMATPHVAG-VAAL--YLQNSATSPASVASAILNGATTGRLSGIG 391

QY 298 LGVPNGQNGRVTLDKSLNVAVYNNSSLSUTSQKATYFTATAGKPLKISLVMSDAPAS 357

Db 392 SGSPN-----RLLYSLSSGS-----GSTAPCT 414

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Qy 358 T-----TASVTLVNDLDLVTAPNGTQY-----VGNDFTSPYNDWNGRN-- 397
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 415 SCsYVTSLSGPGDYNF--QPNGTYYYSAGTHRAWLRGPAAGTDF-DLYLWRWDGSRWL 470
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 398 -----NVENVFINAPQSGTYTIEVOAYN 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 471 TVGSGTGTSEESLSYSGTAGYLLWRIYAYS 501
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
C84120
subtilisin-type proteinase (BC 3.4.21.1-) BH3763 precursor [similarity] - Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C84120
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirano
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C84120
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-757 <STO>
A:Cross-references: UNIPROT:Q9K6G6; UNIPARC:UPI00000C42C2; GB:AP001519; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3763
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-20/Domain: signal sequence #status predicted <SIG>

Query Match 11.5%; Score 259.5; DB 2; Length 757;
Best Local Similarity 22.6%; Pred. No.6.3e-09;
Matches 119; Conservative 58; Mismatches 155; Indels 195; Gaps 20;

Qy 8 VKADVAQHSYGLYGQGIIVADVADTGLDTGRNDSMHEAFRG-----KITALYALG 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 VRGMLDEEGVHLTGKGVKVAVIDTGIDYTHPD--LQSSYKGYDFVDYDDDPMEITASQ 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 58 RTNNANTNGHTHVAGSVLGNSTNGKMAPOANLVFQSIQSDSGGLGLPNLQTLFSQ 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 -----PPTLHGTHVSGIIAANGQV-KGVAPEAEIYARALGPGG--QQTTEQVIAAIEK 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 118 AYSAGARIHTNSGAAANGVATTDTSRNVDDVVRKNDMTILFAAGNKGNGGTISAPGTAK 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 AVEGDGVINLSLGNVTNGPDWPTSLDALDAVEGVAVT-SNGNSGPNMTVVGSPGTSK 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 178 NAITVGAT-----EN--LRPSFGS----- 194
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 287 KATSVGASAPLNTPLYLTARGEENEISLYPSGGGLPWAFKRDLPMDVGYGTEKEWEGVD 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 195 -----YADNINH----- 201
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 347 AEGKVLLIKRGWVPFEKVMHVAAKARGVLIYNNTPGPTGMIEGVNIPVVSITREDG 406
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 202 -----VAQSSRGP-TYDGRIKDDVMAPTFILSARSS 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 407 EFLLEQLEQKNKELTLRTYRKEEDFVALFSRRGPVTHTDVKPDVAVAPGSI----DS 462
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 234 LAPDSSPWANHDSKYAYMGGTSMATPIVAGNVAOLREHFVKNRGITPK--PSLLKAALTA 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 463 TIPNNG-----YLGINTSMAAPHVAGAAALIKQ-----AHPEWTPQVKAALMN 507
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 292 GAADI-----GLGYPNGQGGRVTLDKSLNVAYVYNESSLSQKATYSFTATAGKPLKI 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 508 TAKKLVQDEGVPEIHEQGAGRIQVDRKAV-----AATSLVYPGALSFGK---- 551
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 348 SLVWSDAPASTTASVTL-VNDLDLVIATPAGNTQVVGNDFTSPYNDW 393
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 552 ---WSKDLREKRPVTLTIENHDTV---KTYHILSPDPDQGV 591
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: April 7, 2006, 09:32:40
Job time : 28 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:29:44 ; Search time 114 Seconds
(without alignments)
2685.959 Million cell updates/sec

Title: US-10-820-714a-1-HIS15
Perfect score: 2251
Sequence: 1 NDVARGIVKADVAQHSYGLY.....EVQAYNVPVGPQTFSIAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2242	99.6	Q93UV9_9BACI	Q93UV9 bacillus sp
2	2237	99.4	Q76184_9BACI	Q76184 bacillus sp
3	2178	96.8	Q9AQR3_9BACI	Q9AQR3 bacillus sp
4	2138	95.0	Q9AQR0_9BACI	Q9AQR0 bacillus sp
5	1998.5	88.8	Q9AQR1_9BACI	Q9AQR1 bacillus sp
6	1994.5	88.6	Q9AQR4_9BACI	Q9AQR4 bacillus sp
7	1987.5	88.3	Q9AQR2_9BACI	Q9AQR2 bacillus sp
8	870.5	38.7	Q4NB18_9MICC	Q4NB18 arthrobacte
9	755.5	33.6	Q6MKR4_BDEBA	Q6MKR4 bdellovibri
10	734.5	32.6	Q4NVB5_9DELT	Q4NVB5 anaeromyxob
11	591	26.3	Q4HUY5_GIBZE	Q4HUY5 gibberella
12	590	25.8	Q747P6_GEOSL	Q747P6 geobacter s
13	531.5	23.6	Q54M84_DICDI	Q54M84 dictyosteli
14	523.5	23.3	Q54M83_DICDI	Q54M83 dictyosteli
15	511.5	22.7	TAGC_DICDI	Q8T9W1 dictyosteli
16	497	22.1	TAGB_DICDI	P54683 dictyosteli
17	497	22.1	Q54M83_DICDI	Q54M83 dictyosteli
18	447	19.9	Q9GTN7_DICDI	Q9GTN7 dictyosteli
19	425.5	18.9	Q580L9_9TRYP	Q580L9 trypanosoma
20	414	18.4	Q8U0C9_PYRFU	Q8U0C9 pyrococcus
21	414	18.4	Q5J1Z5_PYRKO	Q5J1Z5 pyrococcus
22	401.5	17.8	Q8RBJ2_THETN	Q8RBJ2 thermoaer
23	393	17.5	Q9FBZ4_STRCO	Q9FBZ4 streptomyce
24	381	16.9	Q8ENV1_OCEIH	Q8ENV1 oceanobacil
25	376	16.2	Q9FC06_STRCO	Q9FC06 streptomyce
26	365	16.2	P95684_STRAO	P95684 streptomyce
27	358.5	15.9	Q82B14_STRAW	Q82B14 streptomyce
28	349	15.5	Q9RL54_STRCO	Q9RL54 streptomyce
29	347.5	15.4	Q9KBJ7_BACHD	Q9KBJ7 bacillus ha
30	346.5	15.4	Q82139_STRAW	Q82139 streptomyce
31	343.5	15.3	Q8KKH6_STRVD	Q8KKH6 streptomyce

32	340	15.1	442	2	Q5L3I5_GEOKA	Q5L3I5 geobacillus
33	338	15.0	412	2	Q9AER6_THEYO	Q9AER6 thermoaer
34	337	15.0	412	2	Q8RC68_THETN	Q8RC68 thermoaer
35	336	14.9	1294	2	Q5OHM7_STRSH	Q5OHM7 streptomyce
36	333	14.8	1237	2	Q8GGT4_STRAZ	Q8GGT4 streptomyce
37	332.5	14.8	442	2	Q65IP4_BACLD	Q65IP4 bacillus li
38	331	14.7	795	2	Q5NW24_9ARCH	Q5NW24 uncultured
39	327.5	14.5	435	2	Q8EMJ3_OCEIH	Q8EMJ3 oceanobacil
40	324.5	14.4	818	2	Q75CG3_BACSP	Q75CG2 bacillus sp
41	324.5	14.4	824	2	Q45464_BACSP	Q45464 bacillus sp
42	323.5	14.4	1220	2	Q9LOAO_STRCO	Q9LOAO streptomyce
43	320.5	14.2	442	2	Q31788_BACSU	Q31788 bacillus su
44	320.5	14.2	891	2	Q93635_THESU	Q93635 thermococcu
45	310.5	13.8	806	1	SUBV_BACSU	P29141 bacillus su

ALIGNMENTS

RESULT 1
Q93UV9_9BACI
ID Q93UV9_9BACI PRELIMINARY; PRT; 640 AA.
AC Q93UV9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Protease.
GN Name=PROF;
OS Bacillus sp. KSM-KP43.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=109322;
RN [1]_TaxID=109322;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KP43;
RA Itoh S., Saeki K.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051423; BAB55674.2; -; Genomic_DNA.
DR PDB; 1WMD; X-ray; A=207-640.
DR PDB; 1WME; X-ray; A=207-640.
DR PDB; 1WMF; X-ray; A=207-640.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67991 MW; 4BBAF77E9D592C15 CRC64;

Query Match	99.6%	Score 2242;	DB 2;	Length 640;
Best Local Similarity	99.8%	Pred. No. 3.1e-138;	Indels 0;	Gaps 0;
Matches 433;	Conservative 0;	Mismatches 1;		
QY	1	NDVARGIVKADVAQHSYGLYGQGIQVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN	60	
Db	207	NDVARGIVKADVAQHSYGLYGQGIQVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN	266	
QY	61	NANDTNGHGHVAGSVLNGSTNGKMAQANLVFQISIMDSGGGLGGLPSNLQTLFSQAYS	120	
Db	267	NANDTNGHGHVAGSVLNGSTNGKMAQANLVFQISIMDSGGGLGGLPSNLQTLFSQAYS	326	
QY	121	AGARHTHSWGAENVGYATTDSRNVDYVYKNDMTILFAAGNEGNNGGTISAPGTAKNAI	180	
Db	327	AGARHTHSWGAENVGYATTDSRNVDYVYKNDMTILFAAGNEGNNGGTISAPGTAKNAI	386	
QY	181	TVGATENLRPSFGSYADNINHVAFQSSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSF	240	
Db	387	TVGATENLRPSFGSYADNINHVAFQSSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSF	446	

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QY 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIIGLY 300
DB 447 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIIGLY 506
QY 301 PNGNQGWGRVTLDKSLNAVYVNESSSLSTSOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNAVYVNESSSLSTSOKATYSFTATAGKPLKISLVMSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGYTIEVQAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGYTIEVQAYN 626
QY 421 VVVGQPTFSLAIVN 434
DB 627 VVVGQPTFSLAIVN 640
RESULT 2
ID Q76L84_9BACI PRELIMINARY; PRT; 640 AA.
AC Q76L84;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Protease.
OS Bacillus sp. KSM-9865.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=192495;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-9865;
RA Okuda M., Saeki K., Kobayashi T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084155; BAC82522.1; -; Genomic_DNA.
DR HSSP; P00782; 1AQN.
DR SMR; Q76L84; 207-640.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67940 MW; 421F7A150FF2868F CRC64;
Query Match 99.4%; Score 2237; DB 2; Length 640;
Best Local Similarity 99.5%; Pred. No. 6.6e-138;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIKVADVAQHSYGLYGQGIQVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIKVADVAQHSYGLYGQGIQVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLNGSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSF 446
QY 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIIGLY 300
DB 447 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIIGLY 506
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QY 301 PNGNQGWGRVTLDKSLNAVYVNESSSLSTSOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNAVYVNESSSLSTSOKATYSFTATAGKPLKISLVMSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGYTIEVQAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNNWNGRNNVNFVINAPOSQGYTIEVQAYN 626
QY 421 VVVGQPTFSLAIVN 434
DB 627 VVVGQPTFSLAIVN 640
RESULT 3
ID Q9AQR3_9BACI PRELIMINARY; PRT; 639 AA.
AC Q9AQR3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Protease.
GN Name=PROA;
OS Bacillus sp. 9860.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133778;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9860;
RX MEDLINE=20568675; PubMed=1118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046403; BAB21266.2; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR3; 206-639.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 639 AA; 68186 MW; 316AF6FFDBE4FF54 CRC64;
Query Match 96.8%; Score 2178; DB 2; Length 639;
Best Local Similarity 96.1%; Pred. No. 4.8e-134;
Matches 417; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
QY 1 NDVARGIKVADVAQHSYGLYGQGIQVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 206 NDVARGIKVADVAQHSYGLYGQGIQVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVLNGSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 266 NANDTNGHGHVAGSVLNGSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 326 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNERPNEGTTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240
DB 386 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSF 445
```

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QY 241 WANHDSKYAYMGCGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 446 WANHDSKYAYMGCGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVGLGY 505
QY 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSQKATYFTATAGKPLKISLWSDAPASTTA 360
DB 506 PNGNQGWGRVTLDKSLNVAIVYNESSLSQKATYFTATAGKPLKISLWSDAPASTTA 565
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYYTIEVOAYN 420
DB 566 SVTLVNDLVLITAPNGTRYVGNDFPAPDNWDGRNNVENVFINSPOSGTYYTIEVOAYN 625
QY 421 VPVGPQTFSLAIVN 434
DB 626 VPVGPQNFSLAIVN 639

RESULT 4
Q9AQR0_9BACI PRELIMINARY; PRT; 434 AA.
AC Q9AQR0_9BACI PRELIMINARY; PRT; 434 AA.
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROG;
OS Bacillus sp. NV1.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133781;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NV1.
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046406; BAB21269.1; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR0; 1-434.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept Bact C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1 1
FT NON_TER 434 434
SQ SEQUENCE 434 AA; 45294 MW; 83517EDDB74125D2 CRC64;

Query Match 95.0%; Score 2138; DB 2; Length 434;
Best Local Similarity 93.3%; Pred. No. 1.2e-131;
Matches 405; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITAYALGRTN 60
DB 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAPRGKITAYALGRTN 60
QY 61 NANTDNGHGHVAGSVLGNSTNKGMAPOANLVFQSDMSGGLGGLPSNLTLFSQAYS 120
DB 61 NANTDNGHGHVAGSVLGNSTNKGMAPOANLVFQSDMSGGLGGLPSNLTLFSQAYS 120
QY 121 AGARITHNSGVAIVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARITHNSGVAIVNGAYTTDSRNVDYVRKNDMAVLFAGNEGPNGGTISAPGTAKNAI 180

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QY 181 TVGATENLRPSFGSVADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
DB 181 TVGATENLRPSFGSVADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
QY 241 WANHDSKYAYMGCGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 241 WANHDSKYAYMGCGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
QY 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSQKATYFTATAGKPLKISLWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSQKATYFTATAGKPLKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTRYVGNDFTPAYDNNWDGRNNVENVFINAPQSGTYYTIEVOAYN 420
QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQNFSLAIVN 434

RESULT 5
Q9AQR1_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR1_9BACI PRELIMINARY; PRT; 433 AA.
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROD;
OS Bacillus sp. SD521.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133780;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SD521.
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046405; BAB21268.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR1; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45576 MW; 98A2DF18F5660DDC CRC64;

Query Match 88.8%; Score 1998.5; DB 2; Length 433;
Best Local Similarity 87.8%; Pred. No. 1.6e-122;
Matches 381; Conservative 28; Mismatches 24; Indels 1; Gaps 1;

QY 1 NDVARGIKVADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITAYALGRTN 60
DB 1 NDVARGIKVADVAQSNYGLYGQGVAVADTGLDTRNDSSMHEAPRGKITAYALGRTN 60
QY 61 NANTDNGHGHVAGSVLGNSTNKGMAPOANLVFQSDMSGGLGGLPSNLTLFSQAYS 120
DB 61 NANTDNGHGHVAGSVLGN-ALNKGMAPOANLVFQSDMSGGLGGLPSNLTLFSQAWN 119

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QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 120 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 179
QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 240
DB 180 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 239
QY 241 WANHSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLIKAALIAGADVGLGY 300
DB 240 WANHSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLIKAALIAGADVGLGY 299
QY 301 PNGNGGWRVTLDKSLNVAYNVNESSLSSTOKATYSFTATAGKPKIKISLVWSDAPASTTA 360
DB 300 PNGNGGWRVTLDKSLNVAYNVNESSLSSTOKATYSFTATAGKPKIKISLVWSDAPASTTA 359
QY 361 SVTLVNDLVLITAPNGTQYVGNDFSTPYNDNWDGRNNVNFVINAPOSQGTITIEVQAYN 420
DB 360 SVTLVNDLVLITAPNGTQYVGNDFSTPYNDNWDGRNNVNFVINAPOSQGTITIEVQAYN 419
QY 421 VPVGPQTFSLAIVN 434
DB 420 VPSGQRFSLAIVH 433

RESULT 6
Q9AQR4_9BACI PRELIMINARY; PRT; 433 AA.
ID Q9AQR4_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR4_9BACI PRELIMINARY; PRT; 433 AA.
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROA;
OS Bacillus sp. D6.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=127889;
RN [1]_TaxID=127889;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=D6;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeiki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.,
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships";
RL Biochem. Biophys. Res. Commun. 279:313-319 (2000).
DR EMBL; AB046402; BAB21265.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR4; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydroxylase; Protease; Serine protease.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 52087E0A2516107F CRC64;

Query Match 88.6%; Score 1994.5; DB 2; Length 433;
Best Local Similarity 87.6%; Pred. No. 2.9e-122;
Matches 380; Conservative 28; Mismatches 25; Indels 1; Gaps 1;

QY 1 NDVARGIVKADVAQHSYGLYGQCIIVAVADTGLDGRNDSSMHFAPRGKITAYALGRTN 60
DB 1 NDVARGIVKADVAQHSYGLYGQCIIVAVADTGLDGRNDSSMHFAPRGKITAYALGRTN 60

QY 61 NANDTNHGHTHVAGSVLGNSTNKGMAPQANLVFQSIMDSGGGLPSNLQTLFSQAYS 120
DB 61 NANDTNHGHTHVAGSVLGN-ALNKGMAPQANLVFQSIMDSGGGLPSNLQTLFSQAWN 119
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 120 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 179
QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 240
DB 180 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 239
QY 241 WANHSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLIKAALIAGADVGLGY 300
DB 240 WANHSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLIKAALIAGADVGLGY 299
QY 301 PNGNGGWRVTLDKSLNVAYNVNESSLSSTOKATYSFTATAGKPKIKISLVWSDAPASTTA 360
DB 300 PNGNGGWRVTLDKSLNVAYNVNESSLSSTOKATYSFTATAGKPKIKISLVWSDAPASTTA 359
QY 361 SVTLVNDLVLITAPNGTQYVGNDFSTPYNDNWDGRNNVNFVINAPOSQGTITIEVQAYN 420
DB 360 SVTLVNDLVLITAPNGTQYVGNDFSTPYNDNWDGRNNVNFVINAPOSQGTITIEVQAYN 419
QY 421 VPVGPQTFSLAIVN 434
DB 420 VPSGQRFSLAIVH 433

RESULT 7
Q9AQR2_9BACI PRELIMINARY; PRT; 433 AA.
ID Q9AQR2_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR2_9BACI PRELIMINARY; PRT; 433 AA.
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROC;
OS Bacillus sp. Y.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133779;
RN [1]_TaxID=133779;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeiki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.,
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships";
RL Biochem. Biophys. Res. Commun. 279:313-319 (2000).
DR EMBL; AB046404; BAB21267.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR2; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydroxylase; Protease; Serine protease.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45588 MW; B81291A803C775AE CRC64;

Query Match 88.3%; Score 1997.5; DB 2; Length 433;
Best Local Similarity 87.3%; Pred. No. 8.2e-122;
Matches 379; Conservative 29; Mismatches 25; Indels 1; Gaps 1;


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QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITIYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITIYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NASDPNGHGHVAGSVLGN-ALNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAWN 119
QY 121 AGARIHTNSWGAANGAYTTDSNRVDDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180
Db 120 AGARIHTNSWGAANGAYTANSRQVDEYVRNNDMTILFAAGNEGPGGTISAPGTAKNAI 179
QY 181 TVGATENLRPPSGSVADNHNHVAQFSSRGPTKGRIPKDPVMAAGTFFILSARSLLAPDSF 240
Db 180 TVGATENLRPPSGSVADNHNHVAQFSSRGATDRGRIKPDVTAAGTFFILSARSLLAPDSF 239
QY 241 WANHDSKVAYMGTSMTATPAGNVAQALREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Db 240 WANYNSKVAYMGTSMTATPAGNVAQALREHFVKNRGITPKPSLLKAALIAAGATDVGLGY 299
QY 301 PNGNOGWRVTLKSLNVAYNSSLSSTSKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 300 PNGDGQGWGRVTLKSLNVAYNSSLSSTSKATYSFTATAGKPLKISLVWSDAPGSTTA 359
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTSFVNDWNGRNNVFNAPQSGTITIEVQAYN 420
Db 360 SVTLVNDLVLITAPNGQYVGNDFTSFVNDWNGRNNVFNAPQSGTITIEVQAYN 419
QY 421 VPGVQPTSLAVN 434
Db 420 VPSGQRFSLAIVH 433

RESULT 8
QANB18_9MICC
ID QANB18_9MICC PRELIMINARY; PRT; 697 AA.
AC QANB18;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin.
GN ORFName=ArthDRAFT_0589;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (PGF-ORN);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHQ1000025; EAL94539.1; -; Genomic_DNA.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
DR HydroLase; Protease; Serine protease.
SQ SEQUENCE 697 AA; 73821 MW; B8924966C67C0714 CRC64;
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Query Match 38.7%; Score 870.5; DB 2; Length 697;
Best Local Similarity 41.4%; Pred. No. 1.8e-48;
Matches 209; Conservative 73; Mismatches 138; Indels 85; Gaps 14;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITIYALGRTN- 59
Db 136 NNVAEILNADVOLNGTYYRGAGEVAVADTGFDTG-DAANPHPAFTGRVQTYALGRTA 254
QY 60 -NNANDTNGHGHVAGSVLGNSTN-----KGMAPQANLVFQSIIMDSGGGLGGLPSNLQ 112
Db 255 PDKADDPHGHGHVAGSVLGRNSATMGAIESTAPEALLILQSLDPPNGGLGGIPVNLN 314
QY 113 TLFSAQYSAGARIHTNSWGA-AVNGAYTTDSNRVDDYVRKN-DMTILFAAGNEGPGNG--- 167
Db 315 DLFQKTYDDGARKVHTNSWGVGLNLPYDASSREIDFVWNHPDQVICFAAGNDGVDGNSD 374
QY 168 -----GTISAPGTAKNAITVGTATENLR-----PSFGSY-----ADNHNVA 203
Db 375 GTVDSNLSGSAAKNCITVGASESLRKEFTSYTYWPGDFPANPVKRDQANNPDGMV 434
QY 204 QPSSRGPTKGRIPKDPVMAAGTFFILSARSLLAP-DSSFWANHDSKVAYMGTSMTATPIVA 262
Db 435 APSSRGPTKGRIPKDPVMAAGTFFILSARSLLAPMGNTFGTSTDPDLPFFDSGTSMTATPLVA 494
QY 263 GNVAQALREHFVKNRGITPKPSLLKAALIAAGADIGLY-----PNGNOGWRVTLK 314
Db 495 GCAAVLRETLVKNGLNPSAALVKALLVNGADVLPQYNPSPSAGESPNSGNGRNVNLAR 554
QY 315 SLNV-----AVNNESSLSSTSKATYSF-----TATAGKP 344
Db 555 SVLPQPGNAGLGGEGGLEQOQEDSFIDIPPEVPKVAAGRRNRGPAEALTAAGVT 614
QY 345 LKISLVSDAPASTTASVTLVNDLVLITAPNGTOYVGNDFTSFVNDWNGRNNVFN 404
Db 615 LKITLVMSDPPGP-----QLQNDLVLILADGSRHSGNSGTTA---GPDNRNNVEQVLW 666
QY 405 NAPSQSGTITIEVQAYNVPVGPQTF 429
Db 667 TGMPPGQARIIVVRAFRITQFPQPYA 691

RESULT 9
Q6MKR4_BDEBA
ID Q6MKR4_BDEBA PRELIMINARY; PRT; 711 AA.
AC Q6MKR4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Subtilisin-like serine protease precursor.
GN OrderedLocNames=Bd2321;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.B., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; EX842652; CAE80143.1; -; Genomic_DNA.
DR HSP; F27693; 1A2.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
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[illegible]

RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=PCA / ATCC 51573;
RX	PubMed14671304; DOI=10.1126/science.1088727;
RA	Meche B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA	Heidelberg J.P., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA	Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA	Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA	Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA	Weidman J.F., Khouri H.M., Feldblum T.V., Utterback T.R.,
RA	Van Aken S.E., Lovley D.R., Fraser C.M.;
RT	"Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT	environments.";
RL	Science 302:1967-1969(2003).
DR	EMBL; AE017180; AAR36610.1; -; Genomic_DNA.
DR	HSSP; P27693; LAH2.
DR	TIGR; GSU3219; -.
DR	GO; GO:0004289; F:subtilase activity; IEA.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPRO11635; APHP.
DR	InterPro; IPRO03961; FN III.
DR	InterPro; IPRO00209; Pept_S8_S53.
DR	Pfam; PF07705; CARDB; 8.
DR	Pfam; PF00041; fn3; 1.
DR	Pfam; PF00082; Peptidase_S8; 1.
DR	PRINTS; PR00723; SUBTILISIN.
DR	PROSITE; PS00137; SUBTILASE_HIS; 1.
KW	Complete proteome.
SQ	SEQUENCE 2030 AA; 207213 MW; ED7ADC27DDB141E01 CRC64;
Query Match	25.8%; Score 580; DB 2; Length 2030;
Best Local Similarity	34.6%; Pred. No. 7.Se-29;
Matches 156; Conservative	69; Mismatches 168; Indels 62; Gaps 15;
Qy	18 GLYGQGQIVAVDTGLD-----TGRNDSSMHEAFRGKITALYALGRTNNANDNTNGH 68
Dd	225 GITGAGQIVGIUSGVDDYDMFPADPNGALPGFCHRIKV-----YDATLGDNHVDVGH 279
Qy	69 GTHVAGSVLGN----GSTNKGMQAQANLVFSIMDSGGGLGLPSNLQTLFSQAYSAGARI 125
Dd	280 GTTHIAGTICDGRPGMPGNGIAPGARIHVQDLVGTGDTLTG-SLELETVLKKAIDSGARI 338
Qy	126 HTWSGAANGVAYTTDSRNVDYV-RKDWTILFAAGNEGPNGCTISAPGTAKNAVITVGA 184
Dd	339 FNGSWGVD--SGNYDALAAALDDFSWRHKDFLAVPFANGNGPBQBOTSPAIKNATSWVA 397
Qy	185 TENLRPSFGSYADINHNHVAOFSRRGPTKGRIKPDVNMAPGTFILSARSLLAPDSFFWANH 244
Dd	398 TGN-----GITDAAT---VSAESSVGQAPDGRANPSVCAPGQGVVSARS----DGLLSGN 445
Qy	245 DSKYVYGGTSMATPIPVAGNVAQLREHF-----VKNRGITPKPSLLKAALINGAA 294
Dd	446 SGTMA-MSGTSVAAAVTSGAAALIROYFTDGFFPTGSFVATNKLQPASALLKAVLVNSAE 504
Qy	295 -----DIGLGYPNGNGOGWRTLDKSI-----NVAYVNESSLSISQKATYSFTATAG 342
Dd	505 ALLSDDPGDCSPKRGGWGAPKLIINTLFNFGDHSLSLEVVDGGTGLETGWVQRLYFPSGG 564
Qy	343 KPLKILSVMSDAPASTTASVTLVNDLDLVITAPNGTOYGVNGDFTSPYND-----NWDGR 396
Dd	565 RLKILTIATWDAAPAACATSPLNDNLNVVAPDGTITYLNDLNCSHGDYESRTGGFSDR 624
Qy	397 NNV-ENVFINAPOSGYTIEVQAYNPVPGQTFSIAI 432
Dd	625 VNYEEQVIKKRPVAGTYLVKVIKAGISIPVGPQPALVM 661

RESULT 13	
Q54M84 DICDI	
ID Q54M84; DICDI PRELIMINARY;	PRT; 1741 AA.
AC Q54M84;	
DT 13-SEP-2005 (TrEMBLrel. 31, Created)	
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)	

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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Name=tagC; ORFNames=DD0191192;
GN Dictyostelium discoideum (Slime mold).
OS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Barriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tuggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhrou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Church C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegod H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFI01000133; EAL64353.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR011140; ABC TM transp.
DR InterPro; IPR003439; ABC transp like.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00864; ABC membrane_1.
DR Pfam; PF00005; ABC tran; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00929; ABC TMIF; 1.
DR PROSITE; PS00211; ABC TRANSPORTER 1; 1.
DR PROSITE; PS00893; ABC TRANSPORTER 2; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR SEQUENCE 1741 AA; 193884 MW; 44DEC61D68E4947D CRC64;

Query Match 23.6%; Score 531.5; DB 2; Length 1741;
Best Local Similarity 28.1%; Pred. No. 9.1e-26;
Matches 166; Conservative 81; Mismatches 149; Indels 195; Gaps 24;

QY 19 LYGGQGVAVAVDTGDTGR---NDS-----SMHEAFRGKITALYALGRITNANDTNGH 68
DB 314 LRKGQGLISADTGLDGGCHFFSDSKYPIPLNSVLNHR-KVVTYITTSDDSDKVDGH 372
QY 69 GTHVAGSVLGL-----NGSTNKGNAPQANLVFQSIMDSGGGLGLI--PSNLQTLFSQAY 119
DB 373 GTHICGSRAGTPEDSSVNISSFSGLATDAKIAF---FDLASGSSSLTPPSDLKQLYQPLY 429
QY 120 SAGARIHTNSWGA-----AVNGAYTTDSRVNVDYVRKN-DMTILFPAAGNPGNGGTIS--A 172
DB 430 DAGARVHCDSWGSVSVEGTGYSSTASIDDFLTHPDPFIILRAAGN---NEQYLSLIT 486

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QY 173 PGTAKNAITVGATENLR-----PSFGSYADNI----- 199
DB 487 QSTAKNVITVGAHQTIHENYLTDCPNYINYOSSVDINQELICDFDSRYCNVYTTACCCLES 546
QY 200 -----NHVAQFSRGPTKDGRIKPDVMAQGTFTIL 228
DB 547 NATTGLASCCPTLLRKSVIDAANTQPLLYNNENNICFSKSGFTHDGRMKPDLVAFGEYIT 606
QY 229 SARSSLA-----PDSSEFWAHDHDKYAYMGGTSMATPIVAGNVAAQLREH-----F 272
DB 607 SARGNGANTQCGDGLS-PTNALLA-IGSTSMATSPAAAATTLIRQVLVDGYVPTGSI 664
QY 273 VNRGITPKPSLLKAALTAGA-----ADIGLGPNGN-----QWGRVT 311
DB 665 VESNKLQPTGSLKALMINNAQLLNGTFLITSSSITYPSNQVFENFAGASLVQMGGAIR 724
QY 312 LDKSLNAVYVNESS-----SLSTSOKATYSFT-- 338
DB 725 MSNHLVHVVNNNNNNNNNTSGITKVFVIGIGLDLRLVKNQWKEESLSTGQNTSYCFITYK 784
QY 339 -----ATAGKPLK---ISLVMSDAPASTTASVTLVNDLDLVI-----TAPNGT 378
DB 785 PSSSSSSGNNIPRVVATLVWTDPPSYAGAKFNVLNLDLTMIYYRDNGSTIFYSNQGS 844
QY 379 QYVGNDFTSYPNDNWDGRNNVENVFINAPOSQTYTIEVOAYNVVPGPQTF 429
DB 845 SPLG---LAPTQDT---LNNVEGIVHNPTPTMPTFRMVAGTNVPMGPQNFS 889

RESULT 14
TAGC_DICDI STANDARD; PRT; 1743 AA.
AC Q23868;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prestalk-specific protein tagC precursor (EC 3.4.21.-).
GN Name=tagC;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=97140317; PubMed=8986798; DOI=10.1073/pnas.93.26.15260;
RA Shaulsky G., Escalante R., Loomis W.F.;
RT "Developmental signal transduction pathways uncovered by genetic suppressors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
CC -!- FUNCTION: Intercellular communication via tagC may mediate integration of cellular differentiation with morphogenesis (By similarity).
CC -!- SIMILARITY: Contains 1 ABC transmembrane type-1 domain.
CC -!- SIMILARITY: Contains 1 ABC transporter domain.
CC -!- SIMILARITY: Contains 1 peptidase S8 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; U60086; AAB03331.1; -; mRNA.
DR EIR; T18279; T18279.
DR HSP; P08716; LMT0.
DR DictyBase; DDB0001795; tagC.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC TM transp.
DR InterPro; IPR003439; ABC transp like.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00864; ABC membrane_1.
DR Pfam; PF00005; ABC tran; 1.

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DR Pfam: PF00082; Peptidase S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000006; ABC_TRANSPORTER; 1.
 DR PROSITE; PS00929; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_2; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 DR PROSITE; PS00136; SUBTILASE ASP; FALSE_NEG.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; FALSE_NEG.
 DR ATP-binding; Glycoprotein; Hydrolase; Nucleotide-binding; Protease;
 KW Serine protease; Signal; Transmembrane; Transport.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 1743 Prestalk-specific protein tagC.
 FT TRANSMEM 962 982 Potential.
 FT TRANSMEM 1027 1047 Potential.
 FT TRANSMEM 1072 1092 Potential.
 FT TRANSMEM 1157 1177 Potential.
 FT TRANSMEM 1260 1280 Potential.
 FT TRANSMEM 1288 1308 Potential.
 FT DOMAIN 1031 1314 ABC transmembrane type-1.
 FT DOMAIN 1450 1687 ABC transporter.
 FT NP_BIND 1485 1492 ATP (Potential).
 FT REGION 316 642 Serine protease.
 FT COMBIAS 42 46 Poly-Asn.
 FT COMBIAS 94 103 Poly-Asn.
 FT COMBIAS 643 646 Poly-Ala.
 FT COMBIAS 733 741 Poly-Asn.
 FT COMBIAS 786 792 Poly-Ser.
 FT COMBIAS 1337 1340 Poly-Glu.
 FT COMBIAS 1346 1352 Poly-Gly.
 FT COMBIAS 1353 1357 Poly-Asn.
 FT COMBIAS 1358 1364 Poly-Asp.
 FT COMBIAS 1381 1386 Poly-Asn.
 FT COMBIAS 1707 1729 Poly-Asn.
 FT ACT_SITE 325 325 Charge relay system (By similarity).
 FT ACT_SITE 372 372 Charge relay system (By similarity).
 FT ACT_SITE 637 637 Charge relay system (By similarity).
 FT CARBOHYD 390 390 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 547 547 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 614 614 N-linked (GlcNAc..). (Potential).
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 FT CARBOHYD 735 735 N-linked (GlcNAc..). (Potential).
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 FT CARBOHYD 1454 1454 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 1704 1704 N-linked (GlcNAc..). (Potential).
 SQ SEQUENCE 1743 AA; 194146 MW; 12DB363E2F729839 CRC64;
 Query Match 23.3%; Score 523.5; DB 1; Length 1743;
 Best Local Similarity 27.9%; Pred. No. 3.1e-25;
 Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;
 QY 19 LYGGQGIIVADTGLDTGR---NDS-----SMHEAFRGKITALVALGRNTNANDTNGH 68
 DB 314 LRKGQGLSIADTGLDGSCHFFDSKYPIPLNSVNLNR-KVVTYTTTSDSDSKVDGH 372
 QY 69 GTHVAGSVLGL-----NGSTKNGMAPQANLVFQSTMDSGGLGGH--PSNLQTLFSQAY 119
 DB 373 GTHICGSAAGTPEDSSVNISSFSGSLATDAKIAF---FDLASGSSSLTPPSDLKQLYQPLY 429
 QY 120 SAGARIHTNSWGA-----AVNGATYTSRNVDDIVRKN-DWTLFPAAGNPGNGGTIS--A 172
 DB 430 DAGARVHCDSWGSVSEVGTSGYSSTASIDDFLTHPDFFILRAAGN---NEQYLSLIT 486
 QY 173 PGTAKNAITVGATENLR-----PSFGSYADNI----- 199
 DB 487 QSTAKRVITVGAHQTHENYLTGPNYINYSQSSVDINQBELICDFDSRYCNYTTAQCCLRS 546

QY 200 -----NHVAQFSSRGPTKDGRIKPDVMAQCTFIL 228
 DB 547 NATTTGLASCCPTLLRRKSVIDAANTOPLLYNENNICSFSSKGPTRDGRMKPALVAPGEYIT 606
 QY 229 SARSSILA-----PDSSFWANHSKYAYMGSTMATPIVAGNVAQREH-----F 272
 DB 607 SARSGCANTTDQCGDGLS-PNTNALLA-ISGTSMATSFAAATATILRLQYLVQDYPTGSI 664
 QY 273 VKNRGITPKPSLLKALAIAGA-----ADIGLYGYPNGN-----QGWGRVT 311
 DB 665 VESNKLQPTGSLKALMINNAQLNGTFQITSSSITYPSNOVFENFAGASLVQGWGAIR 724
 QY 312 LKSLNVAIVNESS-----SLSTSOKATYSFT-- 338
 DB 725 MSNWLHVNNNNNNNNNNKTSDGITKPDGIGGLDLRLVKPNQWKESLSTGQNTSYCFTYK 784
 QY 339 -----ATACKPLK---ISLWSDAPASTTASVTLVNDLQV-----TAPNGT 378
 DB 785 PSSSSNSGNNIPRVVATILVTDPSYAGAKFNVLNNLDLTMYYRDNGSTIFYSNQGS 844
 QY 379 QYVGNDFTPSYNDNMWGRNVFNAPQSGTYTIEVOAYNPVGPQTF 429
 DB 845 SFLG---LAPTQDT---LNNVEGIVHNPTPEPTYRPMWAGTNVPMGPQNF 889
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 Q8T9W1 DICDI PRELIMINARY; PRT; 1825 AA.
 AC Q8T9W1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Serine protease/ABC transporter TagD (ABC transporter B family protein).
 GN Name:tagD; ORFNames=DOB0191427;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RL Anjard C., Loomis W.F.; and the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A., Xu Q.,
 RA Sungang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Deany B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., Van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Loulaeged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstock G., Roenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.P., Platzler B., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kupe A.,
 RT "The genome of the social amoeba Dictyostelium discoideum.";
 RL Nature 0:0-0(2005).
 DR EMBL; AF466309; AAL74253.1; -; Genomic DNA.
 DR EMBL; AAF01000133; EAL64354.1; -; Genomic DNA.
 DR HSSP; P08716; 1MT0.
 DR DictyBase; DDB0191427; tagD.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.

Search completed: April 7, 2006, 09:31:50
Job time : 118 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:33:49 ; Search time 82 Seconds
(without alignments)
2211.438 Million cell updates/sec

Title: US-10-820-714A-1-HIS15
Perfect score: 2251
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2242	99.6	434	3	US-09-985-689A-1
2	2242	99.6	434	4	US-10-385-662-2
3	2242	99.6	434	4	US-10-456-479-2
4	2242	99.6	434	4	US-10-837-566-1
5	2242	99.6	434	5	US-10-820-712A-1
6	2242	99.6	434	5	US-10-820-714A-1
7	2242	99.6	640	3	US-09-920-954-6
8	2242	99.6	640	4	US-10-456-479-4
9	2242	99.6	640	4	US-10-784-870-6
10	2242	99.6	640	5	US-10-820-712A-3
11	2242	99.6	640	5	US-10-820-714A-3
12	2237	99.4	434	4	US-10-456-479-11
13	2237	99.4	434	5	US-10-820-712A-14
14	2237	99.4	434	5	US-10-820-714A-15
15	2237	99.4	640	3	US-09-920-954-8
16	2237	99.4	640	4	US-10-784-870-8
17	2186	97.1	434	3	US-09-985-689A-2
18	2186	97.1	434	4	US-10-456-479-10
19	2186	97.1	434	4	US-10-837-566-2
20	2186	97.1	434	5	US-10-820-712A-12
21	2186	97.1	434	5	US-10-820-714A-13
22	2178	96.8	639	3	US-09-920-954-4
23	2178	96.8	639	4	US-10-784-870-4
24	2150	95.5	639	3	US-09-920-954-1
25	2150	95.5	639	4	US-10-784-870-1
26	2150	95.5	640	3	US-09-920-954-2
27	2150	95.5	640	4	US-10-784-870-2

28	2138	95.0	434	3	US-09-985-689A-6	Sequence 6, Appli
29	2138	95.0	434	4	US-10-456-479-15	Sequence 15, Appl
30	2138	95.0	434	4	US-10-837-566-6	Sequence 6, Appli
31	2138	95.0	434	5	US-10-820-712A-22	Sequence 22, Appl
32	2138	95.0	434	5	US-10-820-714A-23	Sequence 23, Appl
33	2125.5	94.4	433	3	US-09-985-689A-7	Sequence 7, Appli
34	2125.5	94.4	433	4	US-10-456-479-16	Sequence 16, Appl
35	2125.5	94.4	433	4	US-10-837-566-7	Sequence 7, Appli
36	2125.5	94.4	433	5	US-10-820-712A-23	Sequence 23, Appl
37	2125.5	94.4	433	5	US-10-820-714A-24	Sequence 24, Appl
38	1998.5	88.8	433	3	US-09-985-689A-5	Sequence 5, Appli
39	1998.5	88.8	433	4	US-10-456-479-14	Sequence 14, Appl
40	1998.5	88.8	433	4	US-10-837-566-5	Sequence 5, Appli
41	1998.5	88.8	433	5	US-10-820-712A-20	Sequence 20, Appl
42	1998.5	88.8	433	5	US-10-820-714A-21	Sequence 21, Appl
43	1994.5	88.6	433	3	US-09-985-689A-3	Sequence 3, Appli
44	1994.5	88.6	433	4	US-10-456-479-12	Sequence 12, Appl
45	1994.5	88.6	433	4	US-10-837-566-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-985-689A-1
; Sequence 1, Application US/09985689A
; Publication NO. US20030022351A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1

Query Match		99.6%	Score 2242;	DB 3;	Length 434;
Best Local Similarity		99.8%	Pred. No. 2e-170;		
Matches 433;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	NDVARGIVKADVAQHSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	60		
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Qy	61	NANDTNGHGTTHAGSVLNGSTNKGMAQANLVFQSIINDSGGGLGGLPSNLQTLFSQAYS	120		
Db	61	NANDTNGHGTTHAGSVLNGSTNKGMAQANLVFQSIINDSGGGLGGLPSNLQTLFSQAYS	120		
Qy	121	AGARLHTNSWGAANVCAVYTTDSRNVDVVRKNDMTILFAAGNENGGGTISAPGTAKNAI	180		
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Qy	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF	240		
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Qy	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVVRGRTTPKPSLLKAAIAGAADIGLY	300		

Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
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Db 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPKLKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOSQGTITIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOSQGTITIEVQAYN 420
QY 421 VPGPQTFSLAIVN 434
Db 421 VPGPQTFSLAIVN 434

RESULT 2

US-10-385-662-2
; Sequence 2, Application US/10385662
; Publication No. US20040002432A1
; GENERAL INFORMATION:
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: SAITO, KAZUHIRO
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: IZAWA, YOSHIFUMI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KOBAYASHI, TOHRU
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: Alkaline protease
; FILE REFERENCE: 234938US0
; CURRENT APPLICATION NUMBER: US/10/385,662
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: JP 2002-081428
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: JP 2002-165987
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: JP 2002-304230
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: JP 2002-304231
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-385-662-2

Query Match 99.6%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 2e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSFS 240
Db 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSFS 240
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Db 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPKLKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOSQGTITIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOSQGTITIEVQAYN 420
QY 421 VPGPQTFSLAIVN 434

QY 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPKLKISLWSDAPASTTA 360
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Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOSQGTITIEVQAYN 420
QY 421 VPGPQTFSLAIVN 434
Db 421 VPGPQTFSLAIVN 434
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; Sequence 2, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700US0
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-456-479-2

Query Match 99.6%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 2e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSFS 240
Db 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSFS 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPKLKISLWSDAPASTTA 360
Db 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPKLKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOSQGTITIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOSQGTITIEVQAYN 420
QY 421 VPGPQTFSLAIVN 434

Db 421 VPVGPQTFSLAIVN 434

|||||

US-10-837-566-1

Sequence 1, Application US/10837566

Publication No. US20040203129A1

GENERAL INFORMATION:

APPLICANT: HATADA, YUJI

APPLICANT: OGAWA, AKINORI

APPLICANT: KAGEYAMA, YASUSHI

APPLICANT: SATO, TSUYOSHI

APPLICANT: ARAKI, HIROYUKI

APPLICANT: SUMITOMO, NOBUYUKI

APPLICANT: OKUDA, MITSUYOSHI

APPLICANT: SAEKI, KATSUHIISA

TITLE OF INVENTION: Alkaline proteases

FILE REFERENCE: 215483USO

CURRENT APPLICATION NUMBER: US/10/837,566

CURRENT FILING DATE: 2004-05-04

PRIOR APPLICATION NUMBER: US/09/985,689A

PRIOR FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: JP P2000-355166

PRIOR FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: JP P2001-114048

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 434

TYPE: PRT

ORGANISM: Bacillus sp.

US-10-837-566-1

Query Match 99.6%; Score 2242; DB 4; Length 434;

Best Local Similarity 99.8%; Pred. No. 2e-170;

Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60

DB 1 NDVARGIVKADVAQHSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGHGTHVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

DB 61 NANDTNGHGHGTHVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARIHNTNSWGAANGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

DB 121 AGARIHNTNSWGAANGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMACTFILLSARSSILAPDSSF 240

DB 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMACTFILLSARSSILAPDSSF 240

QY 241 WANHDSKYAYMGGTSMAPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300

DB 241 WANHDSKYAYMGGTSMAPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300

QY 301 PNGNQGWGRVTLDKSLNVAAYNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360

DB 301 PNGNQGWGRVTLDKSLNVAAYNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 420

DB 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 420

QY 421 VPVGPQTFSLAIVN 434

DB 421 VPVGPQTFSLAIVN 434

RESULT 5

US-10-820-712A-1

Sequence 1, Application US/10820712A

Publication No. US20050026804A1

GENERAL INFORMATION:

APPLICANT: KAO CORPORATION

APPLICANT: Okuda, Mitsuoyoshi

APPLICANT: Izawa, Yoshifumi

APPLICANT: Kobayashi, Tohru

APPLICANT: Koyama, Shingo

APPLICANT: Sato, Tsuyoshi

TITLE OF INVENTION: ALKALINE PROTEASE

FILE REFERENCE: 251701-USO

CURRENT APPLICATION NUMBER: US/10/820,712A

CURRENT FILING DATE: 2004-04-09

PRIOR APPLICATION NUMBER: 2003-106708

PRIOR FILING DATE: 2003-04-10

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.2

SEQ ID NO 1

LENGTH: 434

TYPE: PRT

ORGANISM: Bacillus sp. KSM-KP43

US-10-820-712A-1

Query Match 99.6%; Score 2242; DB 5; Length 434;

Best Local Similarity 99.8%; Pred. No. 2e-170;

Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60

DB 1 NDVARGIVKADVAQHSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGHGTHVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

DB 61 NANDTNGHGHGTHVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARIHNTNSWGAANGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

DB 121 AGARIHNTNSWGAANGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMACTFILLSARSSILAPDSSF 240

DB 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMACTFILLSARSSILAPDSSF 240

QY 241 WANHDSKYAYMGGTSMAPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300

DB 241 WANHDSKYAYMGGTSMAPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300

QY 301 PNGNQGWGRVTLDKSLNVAAYNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360

DB 301 PNGNQGWGRVTLDKSLNVAAYNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 420

DB 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 420

QY 421 VPVGPQTFSLAIVN 434

DB 421 VPVGPQTFSLAIVN 434

RESULT 6

US-10-820-714A-1

Sequence 1, Application US/10820714A

Publication No. US20050214922A1

GENERAL INFORMATION:

APPLICANT: KAO CORPORATION

APPLICANT: Okuda, Mitsuoyoshi

APPLICANT: Kobayashi, Tohru

APPLICANT: Sumitomo, Nobuyuki

APPLICANT: Takimura, Yasushi

APPLICANT: Sato, Tsuyoshi

TITLE OF INVENTION: ALKALINE PROTEASE

RESULT 5

Best Local Similarity 99.8%; Pred. No. 3.4e-170; Mismatches 1; Indels 0; Gaps 0;
Matches 433; Conservative 0;

QY 1 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTCGRNDSSMHEAPRGKITIYALGRTN 60
|||||
Db 207 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTCGRNDSSMHEAPRGKITIYALGRTN 266
|||||
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
|||||
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
|||||
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
|||||
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
|||||
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
|||||
Db 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
|||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
|||||
Db 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
|||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
|||||
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 446
|||||
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAAIAGAADIGLGY 300
|||||
Db 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAAIAGAADIGLGY 506
|||||
QY 301 PNGNOGWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
|||||
Db 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAAIAGAADIGLGY 506
|||||
QY 301 PNGNOGWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
|||||
Db 507 PNGNOGWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 566
|||||
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVQAYN 420
|||||
Db 567 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVQAYN 626
|||||
QY 421 VPVGPTQTFSLAIVN 434
|||||
Db 627 VPVGPTQTFSLAIVN 640
|||||

RESULT 9

US-10-784-870-6
; Sequence 6, Application US/10784870
; Publication No. US20040142837A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUYOSHI
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/10/784,870
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-784-870-6

Query Match 99.6%; Score 2242; DB 4; Length 640;
Best Local Similarity 99.8%; Pred. No. 3.4e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTCGRNDSSMHEAPRGKITIYALGRTN 60
|||||

Db 207 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTCGRNDSSMHEAPRGKITIYALGRTN 266
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 446
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAAIAGAADIGLGY 300
Db 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAAIAGAADIGLGY 506
QY 301 PNGNOGWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNOGWGRVTLDKSLNVAIVNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVQAYN 420
Db 567 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVQAYN 626
QY 421 VPVGPTQTFSLAIVN 434
Db 627 VPVGPTQTFSLAIVN 640
|||||

RESULT 10

US-10-820-712A-3
; Sequence 3, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-3

Query Match 99.6%; Score 2242; DB 5; Length 640;
Best Local Similarity 99.8%; Pred. No. 3.4e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTCGRNDSSMHEAPRGKITIYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTCGRNDSSMHEAPRGKITIYALGRTN 266
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
|||||

Db 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 446
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADIGLY 506
Qy 301 PNGNGGWRVTLDKSLNAVYNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNGGWRVTLDKSLNAVYNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 566
Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFINAPQSGTITIEVQAYN 420
Db 567 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFINAPQSGTITIEVQAYN 626
Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 11

US-10-820-714A-3
; Sequence 3, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697US0
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-3

Query Match 99.6%; Score 2242; DB 5; Length 640;
Best Local Similarity 99.8%; Pred. No. 3.4e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
Qy 61 NANDTNGHGTTHVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARLHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 327 AGARLHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 446
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADIGLY 506
Qy 301 PNGNGGWRVTLDKSLNAVYNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNGGWRVTLDKSLNAVYNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 566

Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFINAPQSGTITIEVQAYN 420
Db 567 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFINAPQSGTITIEVQAYN 626
Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 12
US-10-456-479-11
; Sequence 11, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700US0
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP9865
US-10-456-479-11

Query Match 99.4%; Score 2237; DB 4; Length 434;
Best Local Similarity 99.5%; Pred. No. 5.1e-170;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGTTHVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGTTHVAGSVLNGSTNKGMAQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARLHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 121 AGARLHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQREHFVKRGITPKPSLLKAALIAGAADIGLY 300
Qy 301 PNGNGGWRVTLDKSLNAVYNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNGGWRVTLDKSLNAVYNESSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFINAPQSGTITIEVQAYN 420
Db 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVFINAPQSGTITIEVQAYN 420
Qy 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 13

US-10-820-712A-14
; Sequence 14, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Teuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820, 712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-712A-14

Query Match 99.4%; Score 2237; DB 5; Length 434;
Best Local Similarity 99.5%; Pred. No. 5.1e-170;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSSMHEAPRGKITAYALGRN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSSMHEAPRGKITAYALGRN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARHTNSWGAANVAGYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARHTNSWGAANVAGYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300

QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNDWGRNNVFNAPQSGTYYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNDWGRNNVFNAPQSGTYYTIEVOAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 14

US-10-820-714A-15
; Sequence 15, Application US/10820714A
; Publication No. US2005021492A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Teuyoshi

; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697USO
; CURRENT APPLICATION NUMBER: US/10/820, 714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-714A-15

Query Match 99.4%; Score 2237; DB 5; Length 434;
Best Local Similarity 99.5%; Pred. No. 5.1e-170;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSSMHEAPRGKITAYALGRN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSSMHEAPRGKITAYALGRN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARHTNSWGAANVAGYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARHTNSWGAANVAGYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRRGPTKDGRIKPDVMAPGTIFILSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300

QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNDWGRNNVFNAPQSGTYYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNDWGRNNVFNAPQSGTYYTIEVOAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 15

US-09-920-954-8
; Sequence 8, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGIYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920, 954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509, 814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-8

Query Match	99.4%;	Score 2237;	DB 3;	Length 640;
Best Local Similarity	99.5%;	Pred. No. 8.6e-170;		
Matches 432;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	NDVARGIVKADVAQSHSYGLYGQGI	VAVADTGLDTCGRNDSSMHEAF	RGKITAIYALGRTN 60
DB	207	NDVARGIVKADVAQSHSYGLYGQGI	VAVADTGLDTCGRNDSSMHEAF	RGKITAIYALGRTN 266
QY	61	NANDTNGHGHVAGSVLGNSTNKGMA	POANLVFQSIMDSGGGLGGLPSNL	QTLFSQAYS 120
DB	267	NANDTNGHGHVAGSVLGNSTNKGMA	POANLVFQSIMDSGGGLGGLPSNL	QTLFSQAYS 326
QY	121	AGARIHTNSWGAAVNGAYTTDSRN	VDDYVRKNDMTILFAAGNEGPNGG	TIISAPGTAKNAI 180
DB	327	AGARIHTNSWGAAVNGAYTTDSRN	VDDYVRKNDMTILFAAGNEGPNGG	TIISAPGTAKNAI 386
QY	181	TVGATENLRPSFGSYADNINHVAQ	FSSRGPTKDGRIKPDVMAPGTFIL	SARSSLAPDSSF 240
DB	387	TVGATENLRPSFGSYADNINHVAQ	FSSRGPTKDGRIKPDVMAPGTFIL	SARSSLAPDSSF 446
QY	241	WANHDSKYAYMGGTSMATPIVAGN	VACLREHFVKNRGITPKPSLLKA	ALIAGAADIGLGY 300
DB	447	WANHDSKYAYMGGTSMATPIVAGN	VACLREHFVKNRGITPKPSLLKA	ALIAGAADIGLGY 506
QY	301	PNGNQGWRVTLDKSLNVAIVNESS	SLSTSQKATYSFTATAGKPLKIS	LVWSDAPASTTA 360
DB	507	PNGNQGWRVTLDKSLNVAIVNESS	SLSTSQKATYSFTATAGKPLKIS	LVWSDAPASTTA 566
QY	361	SVTLVNDLVLITAPNGTOYVGNDF	TPSYNDNWDGRNNVNFINAPOSG	TYTIEVQAYN 420
DB	567	SVTLVNDLVLITAPNGTOYVGNDF	TPSYNDNWDGRNNVNFINAPOSG	TYTIEVQAYN 626
QY	421	VPVGPQTFSLAIVN	434	
DB	627	VPVGPQNFSLAIVN	640	

Search completed: April 7, 2006, 09:35:20
Job time : 83 secs

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OM protein - protein search, using sw model

Run on: April 7, 2006, 09:35:35 ; Search time 17 seconds
(without alignments)
796.313 Million cell updates/sec

Title: US-10-820-714A-1-HIS15

Perfect score: 2251

Sequence: 1 NDVARGIVKADVAQHSYGLY.....EQVAYNPVGPOTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
4: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
5: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	285.5	12.7	802	US-10-510-386-2	Sequence 2, Appli
2	253.5	11.3	272	US-11-020-602-236	Sequence 236, Appl
3	253	11.2	874	US-10-510-386-28	Sequence 28, Appl
4	253	11.2	1047	US-10-510-386-200	Sequence 200, Appl
5	248.5	11.0	269	US-11-020-602-6	Sequence 6, Appli
6	244.5	10.9	275	US-11-065-943-54	Sequence 54, Appl
7	244.5	10.9	275	US-11-020-602-3	Sequence 3, Appli
8	232.5	10.3	275	US-11-020-602-4	Sequence 4, Appli
9	230.5	10.2	274	US-11-156-062-14	Sequence 14, Appl
10	229.5	10.2	274	US-11-156-062-12	Sequence 12, Appl
11	228.5	10.2	279	US-11-156-062-23	Sequence 23, Appl
12	228.5	10.2	274	US-11-020-602-5	Sequence 5, Appli
13	228.5	10.2	382	US-11-020-602-2	Sequence 2, Appli
14	225.5	10.0	274	US-11-156-062-4	Sequence 4, Appli
15	225.5	10.0	274	US-11-156-062-8	Sequence 8, Appli
16	225.5	10.0	1052	US-10-020-602-208	Sequence 208, Appl
17	224.5	10.0	274	US-11-156-062-10	Sequence 10, Appl
18	223.5	9.9	274	US-11-156-062-6	Sequence 6, Appli
19	220.5	9.8	274	US-11-156-062-16	Sequence 16, Appl
20	220.5	9.8	274	US-11-156-062-18	Sequence 18, Appl
21	219.5	9.8	274	US-11-156-062-2	Sequence 2, Appli
22	209.5	9.3	280	US-11-020-602-209	Sequence 209, Appl
23	205	9.1	1432	US-10-510-386-218	Sequence 218, App
24	203	9.0	1647	US-11-052-554A-260	Sequence 260, App
25	180.5	8.0	740	US-11-096-568A-24714	Sequence 24714, A

26	180.5	8.0	777	7	US-11-096-568A-24713	Sequence 24713, A
27	180.5	8.0	790	7	US-11-096-568A-24712	Sequence 24712, A
28	177	7.9	591	6	US-10-510-386-22	Sequence 22, Appl
29	166	7.4	722	7	US-11-096-568A-31863	Sequence 31863, A
30	166	7.4	757	7	US-11-096-568A-31862	Sequence 31862, A
31	166	7.4	798	7	US-11-096-568A-31861	Sequence 31861, A
32	160	7.1	659	7	US-11-096-568A-17896	Sequence 17896, A
33	160	7.1	671	7	US-11-096-568A-17895	Sequence 17895, A
34	160	7.1	791	7	US-11-096-568A-17894	Sequence 17894, A
35	158.5	7.0	733	7	US-11-096-568A-24028	Sequence 24028, A
36	158.5	7.0	759	7	US-11-096-568A-24027	Sequence 24027, A
37	158.5	7.0	764	7	US-11-096-568A-24026	Sequence 24026, A
38	157.5	7.0	791	7	US-11-096-568A-31251	Sequence 31251, A
39	155	6.9	672	7	US-11-096-568A-31251	Sequence 31251, A
40	155	6.9	680	7	US-11-096-568A-23982	Sequence 23982, A
41	152.5	6.8	794	7	US-11-218-986-2	Sequence 2, Appli
42	152.5	6.8	820	6	US-10-821-234-1176	Sequence 1176, Ap
43	144.5	6.4	617	7	US-11-096-568A-31252	Sequence 31252, A
44	137	6.1	3157	7	US-11-052-554A-142	Sequence 142, App
45	135	6.0	418	7	US-11-096-568A-23984	Sequence 23984, A

ALIGNMENTS

RESULT 1
US-10-510-386-2
; Sequence 2, Application US/10510386
; Publication NO. US2005024922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-2

Query Match		12.7%	Score 285.5;	DB 6;	Length 802;
Best Local Similarity		23.0%	Pred No. 5e-13;		
Matches 143;		Conservative 69;	Mismatches 178;	Indels 231;	Gaps 27;
QY	2	DVARGIVKADVAQHSYGLYGGQIQIVAVADTGLDTGRND-SSMHEAFRGK--ITALYALGR	58		
Db	158	DKSAFFIGADQAWKS-GVTGKGIKVAVIDTGVYTHPDLKNNFPGYKGYDFVNDNDYDPOE	216		
QY	59	TNNANDTNG---HGHVAGSVLNGSTNGKMAPOANLVFQSIWDSGGGLGGLPSNLQTLF	115		
Db	217	TPTGPRGGATDHGTHVAGTIAAQQI-KGVAPATLLAYRVLPGG--SGTTENVIAGI	273		
QY	116	SOAYSAGARIHTNSGAAVNGA-YTTDSRNVDVYRKNDMTILFAAGNEGPNGGTISAPG	174		
Db	274	EKAVADGAKVMNLSLNSLNSPDYATSI--ALDWAAGVAVTNSGNSGPNWTVGSPG	331		
QY	175	TAKNAITVGTATE-----NLRPSFGS-----	194		
Db	332	TSRVAISVGSQLPYNEYSVTLPSSYSAKVMGYQBEKDLALNGQSVLVEAGLGQADD	391		
QY	195	-----YADNINH-----	201		
Db	392	SGKDVKGKVAIVQGVIPFVDKAKNAKNAGATCAVIYNNATGEIEANVMGMAVPTVKLSK	451		
QY	202	-----VAQFSRGPTKD-GRIKPDVMAPGTFILSA	230		

Db 452 BEGEKLVQIQKEGRHSVVFSEFKLDKLGTTIASFSRSGPVMDDTMMIKPDVSAAGVNIYST 511
QY 231 RSSLAPDSSFANWHDK-----YAYMGGTSMTPIVAGNVAQLREHFVKNRGITP--KPSL 284
Db 512 IPT-----HDPKPYGVSGTGTSMASPHVAGTAAILKQ-----AKPDWTPEQ 554
QY 285 LKAALIAGAADI-----GLGYPNGNOGWRVTLDKSLNVAYNNESS----- 326
Db 555 IKGVLMTAEKLTDENGKPLPHNTGAGSIRIMEALKASSIVTPGSHSVGTFLKDKGQKT 614
QY 327 -----LTSQXA-----TYSFTATACKPLKISLWSD-----APASTT-----ASVTLVNDL 368
Db 615 KQAPTIENLSHRKAYOLEYSFKGTG-----ITVSGTERVVVPANOTGKAAAKVTVNSA 669
QY 369 DLVITAPNGTVVGNDFTSYNDNDWGRNVVE---NVFINAB-----QSGT 411
Db 670 KTKAGTYEGTVYIRE-----DGRKVAEIPILLIVKEPDYPRVTSVTVPEGAKQQA 719
QY 412 YTIEVQAYNVPGPQTFFSLAI 432
Db 720 YTIE--AY-LPGAEELAPLV 737

RESULT 2

US-11-020-602-236
; Sequence 236, Application US/11020602
; Publication No. US20060024764A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
; FILE REFERENCE: GC527C2
; CURRENT APPLICATION NUMBER: US/11/020,602
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 236
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid of
; OTHER INFORMATION: Bacillus lentus and Bacillus amyloliquefaciens
US-11-020-602-236

Query Match 11.3%; Score 253.5; DB 7; Length 272;
Best Local Similarity 32.9%; Pred. No. 2.6e-11;
Matches 85; Conservative 32; Mismatches 94; Indels 47; Gaps 10;
QY 13 AQHSLYGLVGQGIIVAVADTGLDTRNDSSMHEAFRGKITALLYALGRTNNANDTNGHGTIV 72
Db 15 RAHNRGLTSGVKVAVLDTGIST-----HFDLNRGCASFVGP-STDQNGHGTIV 66
QY 73 AGSV--LNGSTNKGMAPOANLVFQSIMDSGGGLPSNLQTLFSQAYSAGARIHTNSW 130
Db 67 AGTIAALNNSIGVLGVAPSAELYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHVNMSL 124
QY 131 GNAVNGAYTDSRNVDDYVRKNDMTILFAAGNEGPN--GTISAPCTAKNAITVGATENL 188
Db 125 GGSGLAAL-----KAAVDKAVAGSVVVAAGNEGTSGSSTVYGPVKYPSVIAVGA---- 176
QY 169 RPSFGSYADNINHAQFSRGPTKDGRIKPDVMAPTFTLSARSSLAPDSSFANWHDSKY 248
Db 177 -----VDSSNQRAFSFSGVP-----ELDWAPG---VSIQSTLP-----GNKY 211
QY 249 AYMGGTSMTPIVAGNVA 266
Db 212 GAYNGTSMASPHVAGAAA 229

RESULT 3

US-10-510-386-28
; Sequence 28, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-28

Query Match 11.2%; Score 253; DB 6; Length 874;
Best Local Similarity 27.2%; Pred. No. 1.3e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;

QY 25 IVAVADTGLDTRNDSSMHEAFRGKI-----TALYALGRTNNANDTNGHGTIVAGSVLG--- 78
Db 447 VIAVVDTGVDHTLADLS-----GSVKDEGYNVYVGRGTADAMDDRGHGTIVSGIITAAQD 500
QY 79 NGSTNKGMAPOANLVFQSIMDSGGGLPSNLQTLFSQAYSAGARIHTNSGAAVNGAY 138
Db 501 NHFSWAGINAYAKILPVKVLDSG--SGDTEQIANGIYIADHGAKVINLSLG-----GPY 554
QY 139 TTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPCTAKNAITVGATENLRPSFGSYADN 198
Db 555 SRVMEYALKYAAASKNVITVAATGNDGVS--EISYPASSKYTLVSGATNNL----- 602
QY 199 INHVAQFSRSGPTKDGRIKPDVMAPTFTLSARSSLAPDSSFANWHDSKYAYMGGTSMAT 258
Db 603 -DLVSDSYNYGKGL-----DMVAPGTDI---PSLVDPGN-----VTYMSGTSMAA 643
QY 259 PIVAGNVAQLREHFVKNRGITPCKPSLLKALITAGAADIGL---GYPNGN----- 304
Db 644 PHVAAAAGLL-----LSQNPSLKPKQIASLLTETTADYAFEQDNPDPYDLIDBPAAQI 698
QY 305 -----QGWGRVTLDKSLNVAYNNESSSLSTSQKATYGTATAGKPLKI 347
Db 699 PGYDFVSGWGLNVFVHAASVPFELNMKVHPLNRHTAVTGTAKSGVTVKI 747

RESULT 4

US-10-510-386-200
; Sequence 200, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 200
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Bacillus licheniformis


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; CURRENT APPLICATION NUMBER: US/11/156,062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 274
; TYPE: PR1
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-11-156-062-12

Query Match          10.2%; Score 229.5; DB 7; Length 274;
Best Local Similarity 30.6%; Pred. No. 1.5e-09;
Matches      86; Conservative    35; Mismatches 107; Indels   53; Gaps    11;

Qy  7 IVKADVAQHSGYGLYGOGQIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRITNNANDTN 66
     :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db  10 LIRADKKVQ-AQGPKGANKVAVLDTGIQASHPLDNVVGG-----ASFVAGEAYNA-DGN 61

Qy  67 GHGTHVAGSV--LNGSTNKGMAPQANLVFQSIMDSGGGLGCLPSNIQTILFSQAYSAGAR 124
     :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db  62 GHGTHVAGTVAAALDNTTGVLGVPASVSASYAKVLDDSSG--SGSYSIGVSGIEWATTNGMD 119

Qy  125 IHTNSGCAAVNGAVTTDSRVDDIVRKNDMTILFAAGNEGNG--GTISAPGTAKNAITV 182
     :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db  120 VINMSLUGGA---SGSTAMKQAVDMNAYARGVVVVAAGAAGNSSGSNTWTIGYPAKYDVIAV 176

Qy  183 GATENLRPSPGSYADINNHVAQFSRRPTKDGRIKPDVMAPGTFILSARSSLAPDSFWA 242
     :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db  177 GA-----VDSNSNRASFSSVG-----AELEWMAFGAGVYSTYPT----- 210

Qy  243 NHPSKYAYMGTSMATPIVAGNVA-----QLREHFVKNR 276
     :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db  211 ---NTVATNGTSMASPHVAGAAAAILSKHPNLSSASQVRNR 248

RESULT 11
US-11-156-062-23
; Sequence 23, Application US/11/156,062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITUENT VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156,062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 379
; TYPE: PR1
; ORGANISM: Bacillus licheniformis
; US-11-156-062-23

Query Match          10.2%; Score 229.5; DB 7; Length 379;
Best Local Similarity 30.2%; Pred. No. 2.2e-09;
Matches      85; Conservative    37; Mismatches 106; Indels   53; Gaps    11;

Qy  7 IVKADVAQHSGYGLYGOGQIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRITNNANDTN 66
     :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
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Db	115	LiRADKQVQ-AQGPKGANVKAVALDGTGQASHPDLNVVGG-----ASFPVAGEAYN-TDGN	166
Qy	67	GHGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSPQAYSAGAR	124
Db	167	GHGTHVAGTVAALDNTTGVLGVAPSVSLYAVKVLNSSG--SGSYSGIVSGIEWATTNGMD	224
Qy	125	IHTNSWGAAVNGAYTTDSRNVDYVRKNDMTIILFAAGNEGPNG--GTISAPGTAKNATV	182
Db	225	VINNSLGGGA---SGSTAMKQAVDNAYARGVGVVVAAGNSGSGTNTTIGYPKDYDSVI	281
Qy	183	GATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWA	242
Db	282	GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT-----	315
Qy	243	NHDSKYAYMGTSMATPIVAGNVA-----QLREHFVKNR	276
Db	316	---NTYATLNGTSMASPHVAGAAALILSKHPNLISASQVRNR	353
RESULT 12			
US-11-020-602-5			
; Sequence 5, Application US/11020602			
; Publication No. US20060024764A1			
; GENERAL INFORMATION:			
; APPLICANT: Estell, David			
; APPLICANT: Harding, Fiona			
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND			
; TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME			
; FILE REFERENCE: GC527C2			
; CURRENT APPLICATION NUMBER: US/11/020,602			
; CURRENT FILING DATE: 2004-12-22			
; PRIOR APPLICATION NUMBER: US 09/500,135			
; PRIOR FILING DATE: 2000-02-08			
; PRIOR APPLICATION NUMBER: US 09/060,872			
; PRIOR FILING DATE: 1998-04-15			
; NUMBER OF SEQ ID NOS: 240			
; SOFTWARE: PatentIn ver. 2.1			
; SEQ ID NO 5			
; LENGTH: 274			
; TYPE: PRT			
; ORGANISM: Bacillus licheniformis			
US-11-020-602-5			
Query Match 10.2%; Score 228.5; DB 7; Length 274;			
Best Local Similarity 30.2%; Pred. No. 1.7e-09;			
Matches 85; Conservative 37; Mismatches 106; Indels 53; Gaps 11.			
Qy	7	IVKADVAQHSYGLYGQGOIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTNANDTN	66
Db	10	LiRADKQVQ-AQGPKGANVKAVALDGTGQASHPDLNVVGG-----ASFPVAGEAYN-TDGN	61
Qy	67	GHGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSPQAYSAGAR	124
Db	62	GHGTHVAGTVAALDNTTGVLGVAPSVSLYAVKVLNSSG--SGSYSGIVSGIEWATTNGMD	119
Qy	125	IHTNSWGAAVNGAYTTDSRNVDYVRKNDMTIILFAAGNEGPNG--GTISAPGTAKNATV	182
Db	120	VINNSLGGGA---SGSTAMKQAVDNAYARGVGVVVAAGNSGSGTNTTIGYPKDYDSVI	176
Qy	183	GATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWA	242
Db	177	GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT-----	210
Qy	243	NHDSKYAYMGTSMATPIVAGNVA-----QLREHFVKNR	276
Db	211	---NTYATLNGTSMASPHVAGAAALILSKHPNLISASQVRNR	248
RESULT 13			
US-11-020-602-2			
; Sequence 2, Application US/11020602			
; Publication No. US20060024764A1			
; GENERAL INFORMATION:			

RESULT 14

Query Match

7

67

125

183

243

RESULT 15

**FUDICALION
GENERAL INFO**

APPLICANT:
APPLICANT:

AFFILIANT: FUEBEL, ANDREW
APPLICANT: Stehr, Regina

```

; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBTILISIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156,062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-11-156-062-8

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[illegible]

Search completed: April 7, 2006, 09:36:00
Job time : 18 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:40:30 ; Search time 29 Seconds
(without alignments)
1237.284 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNPVGPQTFLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*
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- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2247	100.0	434	2	US-09-985-689A-1
2	2247	100.0	640	2	US-09-509-814A-6
3	2247	100.0	640	2	US-09-920-954-6
4	2242	99.8	640	2	US-09-509-814A-8
5	2242	99.8	640	2	US-09-920-954-8
6	2191	97.5	434	2	US-09-985-689A-2
7	2193	97.2	639	2	US-09-509-814A-4
8	2183	97.2	639	2	US-09-920-954-4
9	2155	95.9	639	2	US-09-509-814A-1
10	2155	95.9	639	2	US-09-920-954-1
11	2155	95.9	640	2	US-09-509-814A-2
12	2155	95.9	640	2	US-09-920-954-2
13	2143	95.4	434	2	US-09-985-689A-6
14	2125.5	94.6	433	2	US-09-985-689A-7
15	2125.5	94.6	641	1	US-08-873-479-42
16	1998.5	88.9	433	2	US-09-985-689A-5
17	1994.5	88.8	433	2	US-09-985-689A-3
18	1987.5	88.5	433	2	US-09-985-689A-4
19	1986.5	88.4	433	2	US-09-104-623A-4
20	1986.5	88.4	433	2	US-09-019-532-4
21	1986.5	88.4	433	2	US-09-338-746-4
22	1986.5	88.4	635	1	US-08-873-479-43
23	1581.5	70.4	345	2	US-09-512-251A-10
24	1581.5	70.4	345	2	US-09-515-150A-10
25	1581.5	70.4	345	2	US-09-196-281-13
26	1581.5	70.4	345	2	US-10-336-324-10
27	452.5	20.1	659	2	US-08-894-818B-1

28	452.5	20.1	659	2	US-09-445-472-12	Sequence 12, Appl
29	452.5	20.1	659	2	US-10-090-624-12	Sequence 12, Appl
30	452.5	20.1	659	2	US-09-841-553-1	Sequence 1, Appl
31	414	18.4	412	2	US-09-445-472-1	Sequence 1, Appl
32	414	18.4	412	2	US-10-090-624-1	Sequence 1, Appl
33	414	18.4	522	2	US-08-894-818B-3	Sequence 3, Appl
34	414	18.4	522	2	US-09-445-472-4	Sequence 4, Appl
35	414	18.4	522	2	US-10-090-624-4	Sequence 4, Appl
36	414	18.4	522	2	US-09-841-553-3	Sequence 3, Appl
37	414	18.4	654	2	US-08-894-818B-35	Sequence 35, Appl
38	414	18.4	654	2	US-09-445-472-16	Sequence 16, Appl
39	414	18.4	654	2	US-10-090-624-16	Sequence 16, Appl
40	414	18.4	654	2	US-09-841-553-35	Sequence 35, Appl
41	401	17.8	659	2	US-08-894-818B-5	Sequence 5, Appl
42	401	17.8	659	2	US-09-841-553-5	Sequence 5, Appl
43	346	15.4	520	2	US-09-000-016-7	Sequence 7, Appl
44	346	15.4	520	2	US-09-514-340-7	Sequence 7, Appl
45	346	15.4	734	2	US-09-000-016-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-985-689A-1

; Sequence 1, Application US/09985689A

; Patent No. 6803222

; GENERAL INFORMATION:

; APPLICANT: HATADA, YUJI

; APPLICANT: OGAWA, AKINORI

; APPLICANT: KAGAWA, YASUSHI

; APPLICANT: SATO, TSUYOSHI

; APPLICANT: ARAKI, HIROYUKI

; APPLICANT: SUMITOMO, NOBUYUKI

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHISA

; TITLE OF INVENTION: Alkaline proteases

; FILE REFERENCE: 215483050

; CURRENT APPLICATION NUMBER: US/09/985,689A

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: JP P2000-355166

; PRIOR FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: JP P2001-114048

; PRIOR FILING DATE: 2001-04-12

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 434

; TYPE: PRT

; ORGANISM: Bacillus sp.

US-09-985-689A-1

Query Match 100.0%; Score 2247; DB 2; Length 434;

Best Local Similarity 100.0%; Pred. No. 6.9e-176;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	60
DB	1	NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	60
QY	61	NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS	120
DB	61	NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS	120
QY	121	AGARHTNSWGAANGVAYTTDSNRNDDYVRKNDMTLLFAAGNEGPNNGGTISAPGTAKNAI	180
DB	121	AGARHTNSWGAANGVAYTTDSNRNDDYVRKNDMTLLFAAGNEGPNNGGTISAPGTAKNAI	180
QY	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTILSARSSLAPSSSF	240
DB	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTILSARSSLAPSSSF	240
QY	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAGAADIGLGY	300

Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIIAGAADIGLGY 300
QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGWRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNDRNNVNFVFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNDRNNVNFVFINAPQSGTYYTIEVOAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 2

US-09-509-814A-6

; Sequence 6, Application US/09509814A

; Patent No. 6376227

; GENERAL INFORMATION:

; APPLICANT: TAKAIWA, MIKIO

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHIISA

; APPLICANT: KUBOTA, HIROMI

; APPLICANT: HITOMI, JUN

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SHIKATA, SHITSUM

; APPLICANT: NOMURA, MASAFUMI

; TITLE OF INVENTION: ALKALINE PROTEASE

; FILE REFERENCE: 0327-0832-OPCT

; CURRENT APPLICATION NUMBER: US/09/509,814A

; CURRENT FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: PCT/JP98/04528

; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 640

; TYPE: PRT

; ORGANISM: Bacillus sp.

US-09-509-814A-6

Query Match 100.0%; Score 2247; DB 2; Length 640;

Best Local Similarity 100.0%; Pred. No. 1.2e-175;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLGNSTKNGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLGNSTKNGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFCTFILSARSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFCTFILSARSLAPDSSF 446
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIIAGAADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIIAGAADIGLGY 506
QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGNQGWRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA 566

QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNDRNNVNFVFINAPQSGTYYTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNDRNNVNFVFINAPQSGTYYTIEVOAYN 626
QY 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 3
US-09-920-954-6
; Sequence 6, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-6

Query Match 100.0%; Score 2247; DB 2; Length 640;

Best Local Similarity 100.0%; Pred. No. 1.2e-175;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLGNSTKNGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLGNSTKNGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFCTFILSARSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFCTFILSARSLAPDSSF 446
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIIAGAADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIIAGAADIGLGY 506
QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGNQGWRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNDRNNVNFVFINAPQSGTYYTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNDRNNVNFVFINAPQSGTYYTIEVOAYN 626
QY 421 VPVGPQTFSLAIVN 434

Db 627 VPVGPQTFLAIVN 640
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RESULT 4

US-09-509-814A-8

; Sequence 8, Application US/09509814A

; Patent No. 6376227

; GENERAL INFORMATION:

; APPLICANT: TAKAIWA, MIKIO

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHIISA

; APPLICANT: KUBOTA, HIROMI

; APPLICANT: HITOMI, JUN

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SHIKATA, SHITSUM

; APPLICANT: NOMURA, MASAFUMI

; TITLE OF INVENTION: ALKALINE PROTEASE

; FILE REFERENCE: 0327-0832-OPCT

; CURRENT APPLICATION NUMBER: US/09/509,814A

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: PCT/JP98/04528

; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 640

; TYPE: PRT

; ORGANISM: Bacillus sp.

US-09-509-814A-8

Query Match

Best Local Similarity 99.8%; Score 2242; DB 2; Length 640;

Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAPRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAPRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSSF 446
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506
QY 301 PNGNQGWRVTLDKSLNVAIVNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNQGWRVTLDKSLNVAIVNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFVINAPOSGTYYTIEVQAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFVINAPOSGTYYTIEVQAYN 626
QY 421 VPVGPQTFLAIVN 434
DB 627 VPVGPQNFSLAIVN 640

RESULT 5

US-09-920-954-8

; Sequence 8, Application US/09920954

RESULT 6

US-09-985-689A-2

; Sequence 2, Application US/09985689A

; Patent No. 6803222

; GENERAL INFORMATION:

; APPLICANT: HATADA, YUJI

; APPLICANT: OGAWA, AKINORI

; APPLICANT: KAGEYAMA, YASUSHI

APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483US0
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 434
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-985-689A-2

Query Match 97.5%; Score 2191; DB 2; Length 434;
Best Local Similarity 96.5%; Pred. No. 2.7e-171;
Matches 419; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVNFINAPQSGTYYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTRVGNDFSAFPDNNWDGRNNVNFINSFGSGTYYTIEVQAYN 420
QY 421 VPVGPQTFSLAIYN 434
Db 421 VPVGPQNFSLAIYN 434

RESULT 7
US-09-509-814A-4
Sequence 4, Application US/09509814A
Patent No. 6376227
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT

APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483US0
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 434
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-985-689A-2

Query Match 97.5%; Score 2191; DB 2; Length 434;
Best Local Similarity 96.5%; Pred. No. 2.7e-171;
Matches 419; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVNFINAPQSGTYYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTRVGNDFSAFPDNNWDGRNNVNFINSFGSGTYYTIEVQAYN 420
QY 421 VPVGPQTFSLAIYN 434
Db 421 VPVGPQNFSLAIYN 434

RESULT 7
US-09-509-814A-4
Sequence 4, Application US/09509814A
Patent No. 6376227
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT

CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: JP 9-274570
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 639
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-509-814A-4

Query Match 97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 2.1e-170;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 206 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
Db 266 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 325
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 326 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSF 240
Db 386 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSF 445
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 446 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 505
QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 506 PNGNQGWRVTLDKSLNVAYNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 565
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVNFINAPQSGTYYTIEVQAYN 420
Db 566 SVTLVNDLVLITAPNGTRVGNDFSAFPDNNWDGRNNVNFINSFGSGTYYTIEVQAYN 625
QY 421 VPVGPQTFSLAIYN 434
Db 626 VPVGPQNFSLAIYN 639

RESULT 8
US-09-920-954-4
Sequence 4, Application US/09920954
Patent No. 6759228
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUMI
APPLICANT: NOMURA, MASAFUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT
CURRENT APPLICATION NUMBER: US/09/920,954
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/509,814
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: JP 9-274570

;	PRIOR FILING DATE: 1997-06-08	
;	NUMBER OF SEQ ID NOS: 24	
;	SOFTWARE: PatentIn version 3.0	
;	SEQ ID NO 4	
;	LENGTH: 639	
;	TYPE: PRT	
;	ORGANISM: Bacillus sp.	
US-09-920-954-4		
	Query Match	97.2%; Score 2183; DB 2; Length 639;
	Best Local Similarity	96.3%; Pred. No. 2.le-170;
	Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0	
Qy	1 NDVARGIVKADVAOSSGLYGGQGIIVADVADTGLDTRNDSSMHEAFRQKITALYALGRTN	60
Db	206 NDVARGIVKADVAOSSGLYGGQGIIVADVADTGLDTRNDSSMHEAFRQKITALYALGRTN	265
Qy	61 NANDTNGHGHVAGSVLGGSTNKGMAPOANLVFQSIMDSCGGLGGLPSNLQTLFSQAYS	120
Db	266 NANDTNGHGHVAGSVLGGSTNKGMAPOANLVFQSIMDSCGGLGGLPSNLQTLFSQAFS	325
Qy	121 AGARIHTNSWGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI	180
Db	326 AGARIHTNSWGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI	385
Qy	181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSSLAPDSSF	240
Db	386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSSLAPDSSF	445
Qy	241 WANHDSKYAYNGGTSMTPIVAGNVQAQLREHFVKNRGITPKPSSLKAALIAGAADVLGY	300
Db	446 WANHDSKYAYNGGTSMTPIVAGNVQAQLREHFVKNRGITPKPSSLKAALIAGAADVLGY	505
Qy	301 PNGNQCHGRVTLDKSLNAVYVNESSLSLSQKATYFTATAGPKLISLVWSDAPASTTA	360
Db	506 PNGNQCHGRVTLDKSLNAVYVNESSLSLSQKATYFTATAGPKLISLVWSDAPASTTA	565
Qy	361 SVTLVNDLDELVTAPNGTQVYVNDFTSPYNDNDWGRNNVENVFINAPQSGTYTIEVQAYN	420
Db	566 SVTLVNDLDELVTAPNGTQVYVNDFTSPYNDNDWGRNNVENVFINAPQSGTYTIEVQAYN	625
Qy	421 VPVGPQTFSLAIVN	434
Db	626 VPVGPQTFSLAIVN	639
RESULT 9		
US-09-509-814A-1		
;	Sequence 1, Application US/09509814A	
;	Patent No. 6376227	
;	GENERAL INFORMATION:	
;	APPLICANT: TAKAIWA, MIKIO	
;	APPLICANT: OKUDA, MITSUYOSHI	
;	APPLICANT: SAEKI, KATSUHIISA	
;	APPLICANT: KUBOTA, HIROMI	
;	APPLICANT: HITOMI, JUN	
;	APPLICANT: KAGEYAMA, YASUSHI	
;	APPLICANT: SHIKATA, SHITSUW	
;	APPLICANT: NOMURA, MASAFUMI	
;	TITLE OF INVENTION: ALKALINE PROTEASE	
;	FILE REFERENCE: 0327-0832-OPECT	
;	CURRENT APPLICATION NUMBER: US/09/509,814A	
;	CURRENT FILING DATE: 2000-04-06	
;	PRIOR APPLICATION NUMBER: PCT/JP98/04528	
;	PRIOR FILING DATE: 1998-10-07	
;	PRIOR APPLICATION NUMBER: JP 9-274570	
;	PRIOR FILING DATE: 1997-06-08	
;	NUMBER OF SEQ ID NOS: 24	
;	SOFTWARE: PatentIn version 3.0	
;	SEQ ID NO 1	
;	LENGTH: 639	
;	TYPE: PRT	
;	ORGANISM: Bacillus sp.	

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (89)..(89)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (102)..(102)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (105)..(105)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (128)..(128)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (130)..(130)
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NAME/KEY: misc feature
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OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (189)..(189)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
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OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (306)..(306)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (324)..(324)
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NAME/KEY: misc feature
LOCATION: (369)..(369)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (431)..(431)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (501)..(501)
OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc feature
LOCATION: (531)..(531)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (541)..(541)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (584)..(584)
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NAME/KEY: misc feature
LOCATION: (591)..(591)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (594)..(594)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (595)..(595)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (596)..(596)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (611)..(611)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (632)..(632)
OTHER INFORMATION: Xaa is any amino acid
US-09-920-954-1

Query Match 95.9%; Score 2155; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSSMHEAFRGKITALYALGRTN 60
Db 206 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSSMHEAFRGKITALYALGRTN 265
Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGSLPSNLQTLFSQAYS 120
Db 266 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGSLPSNLQTLFSQAYS 325
Qy 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 326 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 385
Qy 181 TVGATENLRPSFGSYADNINHVAAQFSSRGPTKDGRIKPDVMAFGTILSARSSLAPDSSF 240
Db 386 TVGATENLRPSFGSYADNINHVAAQFSSRGPTKDGRIKPDVMAFGTILSARSSLAPDSSF 445
Qy 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVQNRGITPKPSLLKAALTAGAADIGLY 300
Db 446 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVQNRGITPKPSLLKAALTAGAADIGLY 505
Qy 301 PNGNQGWGRVTLQKSLNVAIYVNESSLSQATYSFTATAGKPLKISLWSDAPASTTA 360
Db 506 PNGNQGWGRVTLQKSLNVAIYVNESSLSQATYSFTATAGKPLKISLWSDAPASTTA 565
Qy 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDKNDGRNNVNFINAPQSGTYTIEVOAYN 420
Db 566 SVTLVNDLVLITAPNGTYXVGNDFKXPXXXNNDGRNNVNFINAPQSGTYTIEVOAYN 625
Qy 421 VPVGPOTFSLAIVN 434
Db 626 VPVGPOTFSLAIVN 639

RESULT 11
US-09-509-814A-2
; Sequence 2, Application US/09509814A
; Patent No. 6376227


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; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (612)..(612)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (633)..(633)
; OTHER INFORMATION: Xaa is any amino acid
US-09-509-814A-2
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Query Match          95.9%; Score 2155; DB 2; Length 640;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAPRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAPRGKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSXGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSWGAANGAYTTDSRNVDYVVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGAYTTDSRNVDYVVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSGSIYADNINHVAQFSSRGPTKDGRIKPDVMAFGTPIISARSLAPDSSF 240
Db 387 TVGATENLRPSGSIYADNINHVAQFSSRGPTKDGRIKPDVMAFGTPIISARSLAPDSSF 446

Qy 241 WANHDSKYAYMGTSWATPIVAGNVLAQLREHFVNRGITPKPSLLKAAIAGAADIIGLY 300
Db 447 WANHDSKYAYMGTSWATPIVAGNVLAQLREHFVNRGITPKPSLLKAAIAGAADXGLGY 506

Qy 301 PNGNCGWRVTLDKSLNVAIVNESSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNCGWRVTLDKSLNVAIVNESSLSTSQKATYFTATAGKPLKISLVWSDAPASTTA 566

Qy 361 SVTLVNDLVLVTPNGTOYVGNDFTSFYNDWMDGRNVENVFINAPQSGTITIEVQAYN 420
Db 567 SVTLVNDLVLVTPNGTXVYGNDFKPPXXNMDGRNVENVFINXQSGTITIEVQAYN 626

Qy 421 VPGVPQTFSLAIVN 434
Db 627 VPGVPQTFSLAIVN 640
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RESULT 12

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US-09-920-954-2
; Sequence 2, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIKA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 640
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; TYPE: PRT
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (48)..(48)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (54)..(54)
; OTHER INFORMATION: Xaa is any amino acid
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; LOCATION: (71)..(71)
; OTHER INFORMATION: Xaa is any amino acid
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; LOCATION: (90)..(90)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (106)..(106)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
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LOCATION: (188)..(188)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (190)..(190)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (195)..(195)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (287)..(287)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (307)..(307)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (325)..(325)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (370)..(370)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (432)..(432)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (502)..(502)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (532)..(532)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (542)..(542)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (585)..(585)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (592)..(592)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (593)..(593)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (595)..(595)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (596)..(596)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (597)..(597)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (612)..(612)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (633)..(633)
OTHER INFORMATION: Xaa is any amino acid
US-09-920-954-2
Query Match 95.9%; Score 2155; DB 2; Length 640;
Best Local Similarity 96.3%; Pred. No. 4.1e-168; Indels 0; Gaps 0;
Matches 418; Conservative 0; Mismatches 16;
1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGTGRNDSMHEAFRGKITALVALGRTN 60
207 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGTGRNDSMHEAFRGKITALVALGRTN 265
61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
267 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNHNHVAQFSSRGPTKDGRIKPDVMAPTGTFILSARSSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNHNHVAQFSSRGPTKDGRIKPDVMAPTGTFILSARSSLAPDSSF 446
QY 241 WANHDSKIAYMGCTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAALITAGAADIGLGY 300
DB 447 WANHDSKIAYMGCTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAALITAGAADIGLGY 506
QY 301 PNGNQGWGRVTLDKSLNVAVYVNESSLSSTSQKATYFTATAGKPLKISLIVSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAVYVNESSLSSTSQKATYFTATAGKPLKISLIVSDAPASTTA 566
QY 361 SVTLVNDLDELITAPNGTQVGNDFTSPPYNDNDGRNNVENVFINAPQSGTYTITIEVOAYN 420
DB 567 SVTLVNDLDELITAPNGTQVGNDFTSPPYNDNDGRNNVENVFINAPQSGTYTITIEVOAYN 626
QY 421 VPVGPQTFSLAIVN 434
DB 627 VPVGPQTFSLAIVN 640
RESULT 13
US-09-985-689A-6
; Sequence 6, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-6
Query Match 95.4%; Score 2143; DB 2; Length 434;
Best Local Similarity 93.5%; Pred. No. 2.3e-167; Indels 0; Gaps 0;
Matches 406; Conservative 19; Mismatches 9;
QY 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGTGRNDSMHEAFRGKITALVALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGTGRNDSMHEAFRGKITALVALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAAPVNGAYTTDSRNVDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNHNHVAQFSSRGPTKDGRIKPDVMAPTGTFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNHNHVAQFSSRGPTKDGRIKPDVMAPTGTFILSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGQNGRVRTLDKSLNVAQVNETSSSTKQATYSFTATAGKPLKLSLWMSDAPASTTA 360
DB 301 PNGQNGRVRTLDKSLNVAQVNETSSSTKQATYSFTATAGKPLKLSLWMSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNDGRNNVNFVFNAPQSGTYTVEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNDGRNNVNFVFNAPQSGTYTVEVOAYN 420
QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 14
US-09-985-689A-7
; Sequence 7, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-7

Query Match 94.6%; Score 2125.5; DB 2; Length 433;
Best Local Similarity 93.5%; Pred. No. 6.2e-166;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQNNFGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANTDNGHGHTHVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQOAYS 120
DB 61 NANTDNGHGHTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFQOAYS 119
QY 121 AGARIHTNSGVAAGVAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 180
DB 120 AGARIHTNSGVAQVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 179
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
DB 180 TVGATENLRPSFGSYADNINHVAQFSRSGPTDRGRKPDVMAPGTFILSARSSLAPDSSF 239
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADIGLY 300
DB 240 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADIGLY 299
QY 301 PNGQNGRVRTLDKSLNVAQVNETSSSTKQATYSFTATAGKPLKLSLWMSDAPASTTA 360

DB 300 PNGQNGRVRTLDKSLNVAQVNETSPLTSQKATYSFTAQAGKPLKLSLWMSDAPGSTTA 359
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNDGRNNVNFVFNAPQSGTYTVEVOAYN 420
DB 360 SLTLVNDLVLITAPNGTKYVGNDFTPSYNDNDGRNNVNFVFNAPQSGTYTVEVOAYN 419
QY 421 VPVGPQTFSLAIVN 434
DB 420 VPVGPQTFSLAIVH 433

RESULT 15
US-08-873-479-42
; Sequence 42, Application US/08873479
; Patent No. 5891701
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan
; APPLICANT: Lynne, Christianson
; TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
; TITLE OF INVENTION: Having Protease Activity
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5891701c No. 5891701disk of No. 5891701th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,479
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 5251.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-873-479-42

Query Match 94.6%; Score 2125.5; DB 1; Length 641;
Best Local Similarity 93.5%; Pred. No. 1.1e-165;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
DB 209 NDVARGIVKADVAQNNFGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 268
QY 61 NANTDNGHGHTHVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQOAYS 120
DB 269 NANTDNGHGHTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFQOAYS 327
QY 121 AGARIHTNSGVAAGVAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 180
DB 328 AGARIHTNSGVAQVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 387
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240

Mon Apr 10 06:49:18 2006

Db	368	TVGATENLRPSFGSYADNINHVAFSSRGPTRDGRIKPDVMAFGTYIILSARSSLPDSSF	447
Qy	241	WANHDSKYAYWGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY	300
Db	448	WANHDSKYAYWGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVGLGF	507
Qy	301	PNGNOGWRVTLDKSLNVAYNNESSLSTSQKATYSFTATAGKPLKISLVMSDAPASTTA	360
Db	508	PNGNOGWRVTLDKSLNVAFNETSPLSTSQKATYSFTAQAGKPLKISLVMSDAPGSTTA	567
Qy	361	SVTLVNDLVLITAPNGTOYVGNDFTSPYNDNWDGNNVNFVFINAPOSQTYTIEVQAYN	420
Db	568	SLTLVNDLVLITAPNGTKYVGNDETAPYDNNWDGNNVNFVFINAPOSQTYTIEVQAYN	627
Qy	421	VPVGPOTFSLAIYN	434
Db	628	VPVSPOTFSLAIYH	641

Search completed: April 7, 2006, 09:41:08
Job time : 30 secs

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2247	100.0	640	2	Q93U9V_9BACI	Q93U9V	bacillus sp
2	2247	99.8	640	2	Q76L84_9BACI	Q76L84	bacillus sp
3	2183	97.2	639	2	Q9AQR3_9BACI	Q9AQR3	bacillus sp
4	2143	95.4	434	2	Q9AQR0_9BACI	Q9AQR0	bacillus sp
5	1998.5	88.9	433	2	Q9AQR4_9BACI	Q9AQR4	bacillus sp
6	1594.5	88.8	433	2	Q9AQR2_9BACI	Q9AQR2	bacillus sp
7	1387.5	88.5	433	2	Q9AQR2_9BACI	Q9AQR2	bacillus sp
8	870.5	38.7	697	2	Q4NB18_9MTCB	Q4NB18	arthrobacte
9	754.5	33.6	711	2	Q6MKR4_9MTCB	Q6MKR4	bdellovibri
10	739.5	32.9	1748	2	Q4NVB5_9DELT	Q4NVB5	anaeromyxob
11	592	26.3	1088	2	Q4HU55_GIBZE	Q4HU55	gibberellia
12	580	25.8	2030	2	Q747P6_GEOSL	Q747P6	geobacter s
13	531.5	23.7	1741	2	Q5AM84_DICDI	Q5AM84	dictyosteli
14	523.5	23.3	1743	1	TAGC_DFCDI	TAGC	dictyosteli
15	511.5	22.8	1825	2	Q8T9W1_DFCDI	Q8T9W1	dictyosteli
16	497	22.1	1905	1	TAGB_DFCDI	TAGB	dictyosteli
17	497	22.1	1906	2	Q5AM83_DICDI	Q5AM83	dictyosteli
18	447	19.9	1752	2	Q5GTN7_DFCDI	Q5GTN7	dictyosteli
19	425.5	18.9	1388	2	Q980L9_9TRYP	Q980L9	trypanosoma
20	414	18.4	654	2	Q8U0C9_PYRKO	Q8U0C9	pyrococcus
21	414	18.4	663	2	Q5J1Z5_PYRKO	Q5J1Z5	pyrococcus
22	406.5	18.1	561	2	Q8RBJ2_THETN	Q8RBJ2	thermoanaer
23	398	17.7	1239	2	Q9FBZ4_STRCO	Q9FBZ4	streptomyce
24	381	17.0	430	2	Q8ENV1_OCRBI	Q8ENV1	oceanobacil
25	376	16.3	1253	2	Q9FC06_STRCO	Q9FC06	streptomyce
26	366	16.3	1102	2	Q95684_STRCO	Q95684	streptomyce
27	363.5	16.2	1208	2	Q82B14_STRAW	Q82B14	streptomyce
28	349	15.5	1245	2	Q9RU54_STRCO	Q9RU54	streptomyce
29	347.5	15.5	444	2	Q9KBJ7_BACHD	Q9KBJ7	bacillus ha
30	346.5	15.4	1139	2	Q82139_STRAW	Q82139	streptomyce
31	346	15.4	1105	2	Q8KKH6_STRDV	Q8KKH6	streptomyce

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QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 506
QY 301 PNGNQGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPKLISLVMSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPKLISLVMSDAPASTTA 566
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNNNDGRNNVENVFINAPOSQGTITIEVOAYN 420
DB 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNNNDGRNNVENVFINAPOSQGTITIEVOAYN 566
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNNNDGRNNVENVFINAPOSQGTITIEVOAYN 420
DB 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNNNDGRNNVENVFINAPOSQGTITIEVOAYN 566
QY 421 VVPGPQTFSLAIVN 434
DB 627 VVPGPQTFSLAIVN 640
QY 421 VVPGPQTFSLAIVN 434
DB 627 VVPGPQTFSLAIVN 640
RESULT 2
Q76L84_9BACI
ID Q76L84_9BACI PRELIMINARY; PRT; 640 AA.
AC Q76L84_
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Protease.
OS Bacillus sp. KSM-9865.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=192495;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-9865;
RA Okuda M., Saeki K., Kobayashi T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBS databases.
DR EMBL; AB084155; BAC82522.1; -; Genomic_DNA.
DR HSSP; P00782; LAQN.
DR SMR; Q76L84; 207-640.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67940 MW; 421F7A150FF2868F CRC64;
Query Match 99.8%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 9e-139; Indels 0; Gaps 0;
Matches 433; Conservative 1; Mismatches 0;
QY 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGTGHVAGSVLNGSTNGKMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGTGHVAGSVLNGSTNGKMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARHTNSWGAANGVAYTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 327 AGARHTNSWGAANGVAYTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFLSARSSLAPDSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFLSARSSLAPDSF 446
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 506
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QY 301 PNGNQGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPKLISLVMSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPKLISLVMSDAPASTTA 566
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNNNDGRNNVENVFINAPOSQGTITIEVOAYN 420
DB 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNNNDGRNNVENVFINAPOSQGTITIEVOAYN 626
QY 421 VVPGPQTFSLAIVN 434
DB 627 VVPGPQTFSLAIVN 640
RESULT 3
Q9AQR3_9BACI
ID Q9AQR3_9BACI PRELIMINARY; PRT; 639 AA.
AC Q9AQR3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Protease.
GN Name=PROA;
OS Bacillus sp. 9860.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133778;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9860;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus sp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046403; BAB21266.2; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR3; 206-639.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 639 AA; 68186 MW; 316AF6FFDBE4FF54 CRC64;
Query Match 97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 6.7e-135;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;
QY 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 206 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGTGHVAGSVLNGSTNGKMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 266 NANDTNGHGTGHVAGSVLNGSTNGKMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARHTNSWGAANGVAYTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 326 AGARHTNSWGAANGVAYTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFLSARSSLAPDSF 240
DB 386 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFLSARSSLAPDSF 445
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QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
|||
DB 446 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 505
|||
QY 301 PNGNCGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
|||
DB 506 PNGNCGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVMSDAPASTTA 565
|||
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSFYNDNWDGRNNVNFVFNAPQSGTYYIEVQAYN 420
|||
DB 566 SVTLVNDLDLVTAPNGTQYVGNDFTSFYNDNWDGRNNVNFVFNAPQSGTYYIEVQAYN 625
|||
QY 421 VVPGPQTFSLAIVN 434
|||
DB 626 VVPGPQTFSLAIVN 639
|||

RESULT 4
Q9AQR0_9BACI PRELIMINARY; PRT; 434 AA.
AC Q9AQR0_9BACI PRELIMINARY; PRT; 434 AA.
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROE;
OS Bacillus sp. NV1.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133781;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NV1;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus sp.: enzymatic properties, sequences, and
RT evolutionary relationships."
RL Biochem. Biophys. Res. Commun. 279:313-319 (2000).
DR EMBL; AB046406; BAB21269.1; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR0; 1-434.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 434
SQ SEQUENCE 434 AA; 45294 MW; 83517EDDB74125D2 CRC64;

Query Match 95.4%; Score 2143; DB 2; Length 434;
Best Local Similarity 93.5%; Pred. No. 1.7e-132;
Matches 406; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
|||
DB 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
|||
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGLGGLPSNLTLSQAYS 120
|||
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGLGGLPSNLTLSQAYS 120
|||
QY 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTLIPAAAGNPGNGGTISAPGTAKNAI 180
|||
DB 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTLIPAAAGNPGNGGTISAPGTAKNAI 180
|||
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41

```
QY 181 TVGATENLRPFGSVADNINHVAFQSSRGPTKDGRIKPDVMAPGTFFILSARSLAPDSSF 240
|||
DB 181 TVGATENLRPFGSVADNINHVAFQSSRGPTKDGRIKPDVMAPGTFFILSARSLAPDSSF 240
|||
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
|||
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
|||
QY 301 PNGNCGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
|||
DB 301 PNGNCGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
|||
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSFYNDNWDGRNNVNFVFNAPQSGTYYIEVQAYN 420
|||
DB 361 SVTLVNDLDLVTAPNGTQYVGNDFTSFYNDNWDGRNNVNFVFNAPQSGTYYIEVQAYN 420
|||
QY 421 VVPGPQTFSLAIVN 434
|||
DB 421 VVPGPQTFSLAIVN 434
|||

RESULT 5
Q9AQR1_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR1_9BACI PRELIMINARY; PRT; 433 AA.
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROD;
OS Bacillus sp. SD521.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133780;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SD521;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus sp.: enzymatic properties, sequences, and
RT evolutionary relationships."
RL Biochem. Biophys. Res. Commun. 279:313-319 (2000).
DR EMBL; AB046405; BAB21268.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR1; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR00209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 45576 MW; 98A2DF18FE660DDC CRC64;

Query Match 88.9%; Score 1998.5; DB 2; Length 433;
Best Local Similarity 87.8%; Pred. No. 5.2e-123;
Matches 381; Conservative 28; Mismatches 24; Indels 1; Gaps 1;

QY 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
|||
DB 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
|||
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGLGGLPSNLTLSQAYS 120
|||
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGLGGLPSNLTLSQAYS 120
|||
```

Qy	121	AGARIHTNSWGAANGVAYTTDSNRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	180
Ds	120	AGARIHTNSWGAANGVAYTTDSNRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	179
Qy	181	TVGATENLRPSFGSVADNININVAOFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF	240
Ds	180	TVGATENLRPSFGSVADNININVAOFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF	239
Qy	241	WANHDSKYAYMGTSWATPIVAGNVAQRLREHFVKNRGITPKPSLLKAALIAGAADIGLY	300
Ds	240	WANYNSKYAYMGTSWATPIVAGNVAQRLREHFVKNRGITPKPSLLKAALIAGAADIGLY	299
Qy	301	PNGNQGWGRVTLDSKLSNVAYNNESSLTSQKATYSFTATACKPLKLSLVMSDAPASTTA	360
Ds	300	PSGDQGWGRVTLDSKLSNVAYNNEATALATGQKATYSFOAQAGKPLKLSLVMTDAPGSTTA	359
Qy	361	SVTLVNDLVLVITAPNGTQYVGNDFTPSVNDNWDGRNNVNFVINAPOSGTITIEVQYN	420
Ds	360	SYTLVNDLVLVITAPNGQYVGNDFSPYDNDWGRNNVNFVINAPOSGTITIEVQYN	419
Qy	421	VPVGPQTFSLAIVN	434
Ds	420	VPSGPQFSLAIVH	433
RESULT 6			
Q9AQR4_9BACI			
ID	Q9AQR4_9BACI	PRELIMINARY;	PRT; 433 AA.
AC	Q9AQR4;		
DT	01-JUN-2001	(TRENBLrel. 17, Created)	
DT	01-JUN-2001	(TRENBLrel. 17, Last sequence update)	
DT	01-MAR-2004	(TRENBLrel. 26, Last annotation update)	
DE	Protease (Fragment).		
CN	Name=PROA;		
OS	Bacillus sp. D6.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_taxid=127889;		
RP	[1]		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=D6;		
RX	MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;		
RA	Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,		
RA	Horikoshi K.;		
RT	"Novel oxidatively stable subtilisin-like serine proteases from		
RT	alkaliphilic Bacillus sp.: enzymatic properties, sequences, and		
RT	evolutionary relationships.";		
RL	Biochem. Biophys. Res. Commun. 279:313-319(2000).		
DR	EMBL; AB046402; BAB21265.1; -; Genomic_DNA.		
DR	HSP; Q45670; LDBI.		
DR	SMR; Q9AQR4; 1-433.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004289; F:subtilase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR007280; Pept_Bact_C.		
DR	InterPro; IPR002029; Pept_S8_S53.		
DR	Pfam; PF00082; Peptidase_S8; 1.		
DR	Pfam; PF04151; PPC; 1.		
DR	PRINTS; PR00723; SUBTILISIN.		
DR	PROSITE; PS00137; SUBTILASE_HIS; 1.		
DR	PROSITE; PS00138; SUBTILASE_SER; 1.		
KW	Hydrolase; Protease; Serine protease.		
FT	NON_TER	1	
FT	NON_TER	433	
SQ	SEQUENCE	433 AA; 45636 MW; 52087E0A2516107F CRC64;	
Query Match			
Best Local Similarity 88.8%; Score 1994.5; DB 2; Length 433;			
Matches 380; Conservative 28; Mismatches 25; Indels 1; Gaps 1			
Qy	1	NDVARGIKADVAOSSGLYGGQITVAVADTGLDGRNDSMHEAFRGKITALYALGRTN	60
Ds	1	NDVARGIKADVAOANYGLYGGQVAVADTGLDGRNDSMHEAFRGKITALYALGRTN	60

Qy	61	NANDTNGHGT	HVAGSVL	NGSGTNKGM	APQANLV	FOSIMDS	GGGLGGL	PSNLQTL	FSQAYS	120	
Db	61	NANDPNGHGT	HVAGSVL	GN-ALNKG	MAPQANLV	FOSIMDS	GGGLGGL	PSNLMTL	FSQAWN	119	
Qy	121	AGARIHNS	WGAAV	NGAYTTD	SRNVDD	VRKND	MTLFAA	GNEGP	NGGTTISAPG	TAKNAI 180	
Db	120	AGARIHNS	WSGAP	VNGAYTAN	SRQVDE	YVRNND	MTLVFAA	GNEGP	NGGTTISAPG	TAKNAI 179	
Qy	181	TVGATENL	RP	FGSYADN	INHVA	OFSSRGP	TGDKRI	KPDV	MAPGTTISAR	SSLAPDSSF 240	
Db	180	TVGATENY	RP	FGSIADN	PNHIA	QFSSRG	ATDGR	IKPDV	APGTTISAR	SSLAPDSSF 239	
Qy	241	WANHDS	KYAYMG	GTSMAT	PIVAG	NVAQ	LRHFP	VKNRG	ITPKP	SLKAA	LIAGAADIGLGY 300
Db	240	WANTNS	KYAYMG	GTSMAT	PIVAG	NVAQ	LRHFP	IKNRG	ITPKP	SLKAA	LIAGATDVGLGY 299
Qy	301	PNGNOG	RVRTL	DKSLN	VAYV	NSSLS	TOKAT	YSFAT	AGKPLK	ISLV	WSDAPASTTA 360
Db	300	PSGQOG	RVRTL	DKSLN	VAYV	NEATL	TGOKAT	YSFQ	TQAGKPLK	ISLV	WTDAPGSTTA 359
Qy	361	SVTLVNDL	DLVITAP	NGPQYV	GNDF	TSPYND	NWGRN	VNVF	INAP	SGT	YTTIEVQAYN 420
Db	360	SYTLVNDL	DLVITAP	NGQYV	GNDF	SYPD	NWGRN	VNVF	INAP	SGT	YTTIEVQAYN 419
Qy	421	VPVGPQ	FTSLA	IVN	434						
Db	420	VPSGPQ	FTSLA	IVH	433						
RESULT 7											
Q9AQR2_9BACI PRELIMINARY; PRT; 433 AA.											
ID	Q9AQR2_9BACI PRELIMINARY; PRT; 433 AA.										
AC	Q9AQR2;										
DT	01-JUN-2001 (TrEMBLrel. 17, Created)										
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)										
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)										
DE	Protease (Fragment).										
GN	Name:PROC;										
OS	Bacillus sp. Y.										
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.										
OX	NCBI_TaxID=133779;										
RN	[1]										
RP	NUCLEOTIDE SEQUENCE.										
RC	STRAIN=Berkely;										
RX	MEDLINE=2056875; PubMed=1118284; DOI=10.1006/bbrc.2000.3931;										
RA	Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,										
RA	Horikoshi K.										
RT	"Novel oxidatively stable subtilisin-like serine proteases from alkaliphilic Bacillus spp.: enzymatic properties, sequences, and evolutionary relationships.";										
RL	Biochem. Biophys. Res. Commun. 279:313-319(2000).										
RK	EMBL; AB046404; BAB21267.1; -; Genomic_DNA.										
DR	HSSP; Q45670; 1DBI.										
DR	SMR; Q9AQR2; 1-433.										
DR	GO; GO:0008233; F:peptidase activity; IEA.										
DR	GO; GO:0042893; F:subtilase activity; IEA.										
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.										
DR	InterPro; IPR007280; Pept_Bact_C.										
DR	InterPro; IPR000209; Pept_S8_S53.										
DR	Pfam; PF000082; Peptidase_58; 1.										
DR	Pfam; PF04151; PPC; 1.										
DR	PRINTS; PR00723; SUBTILISIN.										
DR	PROSITE; PS00137; SUBTILASE_HIS; 1.										
DR	PROSITE; PS00138; SUBTILASE_SER; 1.										
KW	Hydrolase; Protease; Serine protease.										
FT	NON_TER 1										
FT	NON_TER 433										
FT	NON_TER 433										
SEQUENCE	433 AA; 45588 MW; B81291A803C775AE CRC64;										
Query Match 88.5%; Score 1987.5; DB 2; Length 433;											
Best Local Similarity 87.3%; Pred. No. 2.7e-122;											
Matches 379; Conservative 29; Mismatches 25; Indels 1; Gaps 1;											

QY 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NNDTNGHGHVAGSVLNGSTKMGAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NASDPNGHGHVAGSVLNG-ALNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAWN 119
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNPGNGGTISAPGTAKNAI 180
Db 120 AGARIHTNSGAAVNGAYTTANSRQVDEYVRNNDMTILFAAGNPGNSGTISAPGTAKNAI 179
QY 181 TVGATENLPSFGSYADNTHVAQFSRGPTKDGRIKPDVMAPTILSARSSLAPDSSF 240
Db 180 TVGATENYRPSFGSIADNPHIAQFSRGATRGRIKPDVMAPTILSARSSLAPDSSF 239
QY 241 WANHDSKYAYMGTSMTATPVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADICLGY 300
Db 240 WANYNSKYAYMGTSMTATPVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADICLGY 299
QY 301 PNGNQGWGRVTLKSLNVAIVYVNESSLSQKATYSTATAGKPKLSILVMSDAPASTTA 360
Db 300 PNGDQGWGRVTLKSLNVAIVYVNEATATATQKATYSFQAQKPKLSILVMTDAPGSTTA 359
QY 361 SVTLVNDLVLITAPNGTQVGNDFSPYNDWGRNENVENFINAPOSGTYTIEVQAYN 420
Db 360 SVTLVNDLVLITAPNGTQVGNDFSPYNDWGRNENVENFINAPOSGTYTIEVQAYN 419
QY 421 VPVGPOTFSIAIVN 434
Db 420 VPSGPORFSLAIVH 433

RESULT 8

Q4NB18_9M1CC
ID Q4NB18_9M1CC PRELIMINARY; PRT; 697 AA.
AC Q4NB18;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin.
GN ORFNames=ArthDRAFT_0589;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (PGF-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHQ01000025; EAL94539.1; -; Genomic_DNA.
DR InterPro; IPR000209; Pept S8 S53.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 697 AA; 73821 MW; B8924966C67C0714 CRC64;

Query Match 38.7%; Score 870.5; DB 2; Length 697;
Best Local Similarity 41.4%; Pred. No. 1.1e-48;
Matches 209; Conservative 73; Mismatches 138; Indels 85; Gaps 14;
QY 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSSMHEAFRGKITALYALGR- 59
Db 196 NVVAREILNADVLQNGTTRYRGAGEVAVADTGFDTG-DAANPHPAFTGRVQTYALGRTA 254
QY 60 -NNDTNGHGHVAGSVLNGSTN-----KGMAPQANLVFQSIMDSGGGLGGLPSNLQ 112
Db 255 PDKADDPHGHGHVAGSVLGRNSATMGAIETGAPELLILQSLDPPNGGLGIPVNLN 314
QY 113 TLFQSAQYSAGARIHTNSWGA-AVNGAYTTDSRVDDYVRKN-DMTILFAAGNPGNG- 167
Db 315 DLFQKTYDDGARVHTNSWGVGNLNPYDASSREIDFVWNHPDQVLCFAAGNDGVGNSD 374
QY 168 -----GTISAPGTAKNAITVGATENLR-----PSFGSY-----ADNINHVA 203
Db 375 GTVDSNSISGSAKNCITVGASESLRKEFTSYGTYWPGDPANPVKRDQKANNPDGMV 434
QY 204 QFSRGPTKDGRIKPDVMAPTILSARSSLAP-DSSFWANHDSKYAYMGTSMTATPIVA 262
Db 435 AFSSRGPTKEGRIKPDVAPGTSTLSTSRNAPMGNTFGTSTDPLEFFDSGTSMTATPLVA 494
QY 263 GNVQALREHFVKNRGITPKPSLLKAALIAGAADICLGY-----PNGNQGWGRVTLK 314
Db 495 GCAAVLRETILVKNGLNSPSAALVKALLVNGADVLPQYNPSEAGESPNGNSGWRVNLAR 554
QY 315 SLNV-----AYVNESSLSQKATYSF-----TATAGKP 344
Db 555 SVVLPGQPGNAGLGGGPLEQGEDSFITDIEEVKPKVAAGRRNGPAAEPALTAAGVT 614
QY 345 LKISLVMSDAPASTTASVTLVNDLVLITAPNGTQVGNDFSPYNDWGRNENVENFI 404
Db 615 LKISLVMSDPPGP-----QLQNDLVLILVLAADGSRHSGSGTTA---GPDRRNNVQVLW 666
QY 405 NAPSQSGTYTIEVQAYNVVGPQTFS 429
Db 667 TGMPPQGARIVVRAFRITQFPQPYA 691
RESULT 9
Q6MKR4_BDEBA
ID Q6MKR4_BDEBA PRELIMINARY; PRT; 711 AA.
AC Q6MKR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Subtilisin-like serine protease precursor.
OS OrderedLocusNames=Bd2321;
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective."
RL Science 303:689-692(2004).
DR EMBL; BX842652; CAE80143.1; -; Genomic_DNA.
DR HSSP; P27693; IAH2.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; P:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Pept S8 S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.

```
DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Complete proteome; Protease; Signal.
FT SIGNAL 1
SQ SEQUENCE 711 AA; 74914 MW; 4930050843357EE5 CRC64;

Query Match 33.6%; Score 754.5; DB 2; Length 711;
Best Local Similarity 37.9%; Pred. No. 4.8e-41;
Matches 180; Conservative 77; Mismatches 145; Indels 73; Gaps 13;

QY 18 GLYGGOQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRNNA-NTNGHGTHVAGSV 76
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 GYAGRGQTVSMADTGLDSG-NTGATHQDPFAGGVISGYPFGLWSKSWSDPMHGHTHVAGSV 301
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 77 LQNGSTNGM-----APOANLVFQSTMDSGGLGLPSNLQTLFQAYAGARIHTNSMGA 132
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 302 MGRGTASKGLLKGGAEEANVAEGMWSPMKNLSPVSKLGLDFEKAADGARIHTNSMGG 361
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 133 A-VNGAYTTDSRNVDDYVRKN-DMTILFAAGNEGP-----NGGTISAPGTAKNAITV 182
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 362 ARTFCAYDNFAQVDEWSYANPDMILILFAAGNSGADKNKGRIDNSMASPGTAKNVLTV 421
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 193 GATENL-----RPSFGSY-ADNINHVAFSSRGPTKDGRIKPD 219
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 422 GASENVTKSGGIQVPISKLRAAKDEWPSEPIYSYISDNGNGLAMFSSRGPTTDGRTKPD 481
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 VMAPGTFTILSRSLAPDSSFWANHDSKYVYMGGTSMATPIVAGNVAOLREHFVKNGRI- 278
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 482 IVAPGTNVLSVFSQEKDASPLMGAYNKDYVMSGGTSMATPLAAGAAATARQVLVLEKGMK 541
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 279 TPKPSLLKAALITAGAADIGLGY-----PNGNQGRVTLDKSLNVA----- 319
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 542 NPSAALMKATMLHTAVDMYPGQGEIGARGQEIILTRRENSDEGYGRVDVANILGGAT 601
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 320 -YVNESSLSQKATYSTATAGPKLKSILWSDAPASTTASVTLVNDLDTLVIITAPNGT 378
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 602 QFVDRNQVQAQVAGSVSEYFTLNAPGSLYANLVMTDAPGSANAQAALVNDLDTLVLTPNGQ 661
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 379 QIVGVNDFTSPYNDNWDGRNVNFINAPQSGTYTIEVQAYNPV- -GPQTFSL 430
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 662 TLMSMDHI-----NNLEWIEKSLPAGTYKLVTKVFKVPQKGQAQAYAL 706
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q4NVB5_9DELIT PRELIMINARY; PRT; 1748 AA.
AC Q4NVB5;
DT 13-SEP-2005 (TremBLrel. 31, Created)
DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin, Nepovirus coat
DE protein, N-terminal: Nepovirus coat protein, N-terminal precursor.
GN ORFNames=AdehDRAFT 3007;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RL dehalogenans 2CP-C.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RL dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD01000011; EAL79523.1; -; Genomic_DNA.
KW Capsid protein; Signal.
FT SIGNAL 1
SQ SEQUENCE 1748 AA; 177411 MW; B1E6DE33BE81DE76 CRC64;

Query Match 32.9%; Score 739.5; DB 2; Length 1748;
Best Local Similarity 40.1%; Pred. No. 1.5e-39;
Matches 192; Conservative 66; Mismatches 154; Indels 67; Gaps 19;

QY 1 NDVARGIVK----ADVAQSSYGLYGGQIIVAVADTGLD-----TGRNDSSMHEAFR 47
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 248 NDTSRWTIQTQYSPDSITSIDRGLDGRGQIIVAGTGLDHDACWFRDPICAAAGPMHR--- 304
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 48 GKITALYALGRTNANDTN-GHGTHVAGSVLGN-----GSTNKGMAQANLVFOSIMDS 100
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 305 -KVAAYLTVG--GDDYDGNLGHGTHVAGTVAGDQPTITGGAAANGMAPGARVVVTTDLFLG 361
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 101 GGLGLPSNLQTLFQAYAGARIHTNSWGAANVAGYTTDSRNVDDYVRKN-DMTILFA 159
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 362 ENWFSPADLAIEFTTYPALGARLHTNSWSSN-AYDALARSADRFWHEHPDLVLFA 420
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 160 AGNEGPNGTISAPGTAKNAITVGTATENLRPFGSYADNINHVAFSSRGPTKDGRIKPD 219
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 NGNAGPDVGSVGCAPATAKNVSVGATGN-----GLAED---VASFSSHGPAADGRTKPT 472
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 VMAPGTFTILSRSLAPDSSFWANHDSKYVYMGGTSMATPIVAGNVAOLREHFVKN---R 276
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 473 LTPAGVGIVSADSDGTSPAS---NNCSTVAF-SGTSMATPAAAGAAALVROYFEGGFWPS 527
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 277 GI-----TPKPSLLKAALITAGADI-----GLG-YPNGNOCGRVTLDKSLNVA----- 319
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 528 GLGSPADARSFAALVKATLVNSAQNVAGENGNGPISTGGGKRLNSALRFAADAAY 587
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 320 -YVNESSLSQKATYSTATAGPKLKSILWSDAPASTTASVTLVNDLDTLVIITAPNG 377
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 588 LDVVEVAGLETGGSTFQVSTGAQPLKLTLMVMTDAPGSLADSLVNDLDTLVIITAPNG 647
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 378 -TQYGVNDFT---SPYNDNWDGRNVNFINAPQSGTYTIEVQAYNPVGPQTFSLAI 432
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 648 ATTYLGNVFALGESVAGAPDLNVEEQVLLAAPTGYTVTVRTGYNVVPVGPQFPALVI 706
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q4HUY5_GIBZE PRELIMINARY; PRT; 1088 AA.
AC Q4HUY5;
DT 13-SEP-2005 (TremBLrel. 31, Created)
DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG11223.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Diaz J.S., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Choepl Y., Collymore A., Cook A., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Haggopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
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RA	Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA	Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA	Oliver J., Peterson K., Phunthang P., Pierre N., Purcell S.,
RA	Rachupa A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA	Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA	Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA	Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA	Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA	Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA	Lander E.;
RL	"Fusarium graminearum genome sequence.";
RT	Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC	preliminary data.
DR	EMBL; AACM01000460; EAA75433.1; -; Genomic_DNA.
KW	Hypothetical protein.
SQ	SEQUENCE 1088 AA; 119629 MW; E3B38CB94C07F542 CRC64;
Query Match 26.3%; Score 592; DB 2; Length 1088;	
Best Local Similarity 35.6%; Pred. No. 4e+30;	
Matches 181; Conservative 71; Mismatches 170; Indels 86; Gaps 24;	
Qy	1 NDVARGIVKADVAQSSYGLCYCGQIIVAVATGTLTGTRNDSSM-----HEAFRGKITALVAL 56
Dd	581 NDLAARETLNANILALSITYEGNGQKVCAVDTFDQGKWADEMGFLVHPAENGVRVEHLEAL 640
Qy	57 GRTNANDNTNGHGTHVAGSVLNGSTN-----KGMAPOANLVFSQI-----MDSGGGLGG 106
Dd	641 W-LGDSKDTAGHTHVACISCGNGLYKNGDIRVGRVAPGATLVAQSIAQVSRDENKGAIE 699
Qy	107 LPSNML-QTLFSQAYSAGARIHTNSWGA---AVNG--AYTTDSRNVDYV-RKNDMTILFA 159
Dd	700 VPMDLGQLGFSPNYKLGYRIHSNSGWKVDAKTQGLGYEQAWDIDKFVIDHQDFVLVA 759
Qy	160 AGNEPNGGT-----ISAPGTAKNAITVGATENLRPSFGSYADN-----INHVAQFS 206
Dd	760 AGNNAEKAKSNSNHIGAAGSAFNCTIVGATGTTTPNNNDYFDNEGAKPMTRINDTAKFS 819
Qy	207 SRGPTKD-----GRIKPDVMPAGPTFTLSARS-SLAPDS-----SFWANHDSKYVM 251
Dd	820 SRGTPKEGRDINGNEYAGRIPDVVAPGVAILLSAASRAMAKDSNRVMYGTGDGDDWTFM 879
Qy	252 GGTSMATPIVAGNVQAOLREHFVKRNGITPKPSLLKAALIAGAAD-----IGLGYPNNGN 305
Dd	880 SGTSMSPLVAGCVALLREALKEHGKPKSAALIKALLVNGAVNFSQLGLGLGY-DYDQ 938
Qy	306 GWGRVTLDKSLNV-----AYNESSSLSTSQ-----KATYS-FTATAGK-PL 345
Dd	939 GFGRVDIDSSISMVKLSFSFDGKKLPEDTQFDVAPLRQPVEERRRSTSLIPVPAGRNRL 998
Qy	346 KISLVSDASPASTTASVLTNLDDLVIATPNGTYGVGNDFTPSYNDNMWDGRNNVENVPIN 405
Dd	999 TVTILVPDKFAQ---SGLMQNDINLIIVLS-GGAERHGMKGKP---GYDHTNNVEKLIWE 1051
Qy	406 APOSGTYTIEVQAY-NVPV-CPOTFFSLA 431
Dd	1052 NVPEGETFKIVASIWNINIDVKAPTSSFAVA 1079
RESULT 12	
Q747P6_GEOSL	
ID	Q747P6_GEOSL PRELIMINARY; PRT; 2030 AA.
AC	Q747P6_
DT	03-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Fibronectin type III domain protein.
GN	OrderedLocusNames=GSU3219;
OS	Geobacter sulfurreducens
OC	Bacteria; Proteobacteria; Deltaaproteobacteria; Desulfuromonadales;
OC	Geobacteraceae; Geobacter.
OX	NCBI TaxID=35554;

[1]
 NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Mehe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkman L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Davidesen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments.";
 RL Science 302:1967-1969(2003).
 DR EMBL; AE017180; AAR36610.1; -; Genomic_DNA.
 DR HSSP; P27693; 1AH2.
 DR TIGR; GSU3219; -.
 DR GO; GO:0004289; P:subtilase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR011635; APHP.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR000209; Pept_S8_S53.
 DR Pfam; PF07705; CARD8; 8.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 KW Complete proteome.
 SQ SEQUENCE 2030 AA; 207213 MW; ED7ADC27DD141E01 CRC64;
 Query Match 25.8%; Score 580; DB 2; Length 2030;
 Best Local Similarity 34.6%; Pred. No. 5.6e-29;
 Matches 158; Conservative 69; Mismatches 168; Indels 62; Gaps 15;
 QY 18 GLYQCGQIVAVADTGLD-----TGRNDSMHEAFRGKITALYALGRTNNDNTNGH 68
 DB 225 GITGAGQIVGIADSGVDYDMPWFADPNGALPGGCHKIVG-----YDATLGDNDHVDAGH 279
 QY 69 GTHVAGSVLGN-----GSTNKGMAPQANLVFQSIMDSGGGLGLPSNLQTLFSAYSAGARI 125
 DB 280 GTHIAGTICDRGPGMNGIAPGARIHQDLVGTDTLTG-SLELETVLKKAYDSGARI 338
 QY 126 HTNSWGAENVAGYTTDSRNVDYV-RKNDWTILFAAGNPGNGGTTISAPGTAKNAITVGA 184
 DB 339 FNGSWGVD-SGNYDALAAALDDFSWRKDFLAVFANGNGGPAEQTATSPAIAKNATSVVA 397
 QY 185 TENLRSPFSYADNIHNVAFSSRGTKDRIKPDYMACTFTLSARSSLIAPDSSFWANH 244
 DB 398 TGN-----GTDAA-----VSAESSVGQAPGRANPSVGAQGVGSARS-----DGLIGSGN 445
 QY 245 DSKYAVMGGTSMATPIVAGNVAOLRHF-----VKNRGITPKPSLLKKAALAGAA 294
 DB 446 SGTWA-MSGTSVAAVTSAGAAALIRQYFDGFPPTGSPVATNKLQPSAALLKAVLVNSAE 504
 QY 295 -----DIGLYPNGNGWGRVTLDKSL-----NVAYVNESSLSSTSQKATYSFTATAG 342
 DB 505 ALLSDDPGDCSPKSGWGRPKLINTLFFNGDSHSLVVDGGTGLETDGVMQRLYFSPGG 564
 QY 343 KPLKISLVMSDAPASTASVTLVNDLDLIVATPNGTQYVGNDRFTSPYND-----NWDGR 396
 DB 565 RRLUKITLAWDPAAPGATGASPLTNDLNLVVPADGTTGYLGNLNCSHGDYESTRGFSDR 624
 QY 397 NNV-ENVFNAPOSGTYTTEVQAVNVNPVPGPQTFLAI 432
 DB 625 VNVEEQVVKRPVAGYTLVKVIGASIPVGQPPALVM 661
 RESULT 13
 Q54M84_DICD1
 ID Q54M84_DICD1 PRELIMINARY; PRT; 1741 AA.
 AC Q54M84;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

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13-SEP-2005 (TREMELrel. 31, Last annotation update)
DE ABC transporter B family protein.
CN Name=tagC; ORFNames=DDR0191192;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugeng R., Berriman M., Song J., Olsen R., Szafarski K., Xu Q.,
RA Tungkal B., Kummerfeld S., Madera M., Konfortov B.-A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Linday R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louisge H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RL "The genome of the social amoeba Dictyostelium discoideum.";
CC Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data
CC EMBL; AAFI01000133; EAL64353.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00664; ABC membrane; 1.
DR Pfam; PF00005; ABC tran; 1.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
SQ SEQUENCE 1741 AA; 193684 MW; 44DEC61D68E4947D CRC64;

Query Match 23.7%; Score 531.5; DB 2; Length 1741;
Best Local Similarity 28.1%; Pred. No. 7e-26;
Matches 166; Conservative 81; Mismatches 149; Indels 195; Gaps 24;

QY 19 LVQGGQIVAVDTGLDGTGR---NDS-----SMHEAFRGKITALYALGRTNNANDTNGH 68
DB 314 LRKGQILSIADTGLDGSCHFFSDSKYPIPLNSVNLNHR-KVVTYITTSDDSDKVDG 372
QY 69 GTHVAGSVLG-----NGSTNKGMAPOANLVFQSIMDSGGGLGL-PSNLQTLFSQAY 119
DB 373 GTHICGSAAGTPESSSVNLSFSSGLTADAKIAF---FDLASGSSSLTPPSDLKQLYQPLY 429
QY 120 SAGARIHTNSWGA-----AVNGAYTDSRNVDDYVRKN-DMTILFAAGNEGPNGGTIS--A 172
DB 430 DAGARVHCDSWGSVSEGYTGSYSSDTSASIDDFLFTHPDIFILRAAGN--NEQVLSLTL 486

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DR pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD00006; ABC transporter; 1.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC TRANSPORTER_2; 1.
DR PROSITE; PS00893; SUBTILASE ASP; FALSE_NEG.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00137; SUBTILASE_SER; 1.
DR PROSITE; PS00138; SUBTILASE_SER; FALSE_NEG.
KW ATP-binding; Glycoprotein; Hydrolase; Nucleotide-binding; Protease;
KW Serine protease; Signal; Transmembrane; Transport.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 1743 Prestalk-specific protein tag.
FT TRANSMEM 962 982 Potential.
FT TRANSMEM 1027 1047 Potential.
FT TRANSMEM 1072 1092 Potential.
FT TRANSMEM 1157 1177 Potential.
FT TRANSMEM 1260 1280 Potential.
FT TRANSMEM 1288 1308 Potential.
FT DOMAIN 1031 1314 ABC transmembrane type-1.
FT DOMAIN 1450 1687 ABC transporter.
FT NP_BIND 1485 1492 ATP (Potential).
FT REGION 316 642 Serine protease.
FT COMBIAS 42 46 Poly-Asn.
FT COMBIAS 94 103 Poly-Asn.
FT COMBIAS 643 646 Poly-Ala.
FT COMBIAS 733 741 Poly-Asn.
FT COMBIAS 786 792 Poly-Ser.
FT COMBIAS 1337 1340 Poly-Glu.
FT COMBIAS 1346 1352 Poly-Gly.
FT COMBIAS 1353 1357 Poly-Asn.
FT COMBIAS 1358 1364 Poly-Asp.
FT COMBIAS 1381 1386 Poly-Asn.
FT COMBIAS 1707 1729 Poly-Asn.
FT ACT_SITE 325 325 Charge relay system (By similarity).
FT ACT_SITE 372 372 Charge relay system (By similarity).
FT ACT_SITE 637 637 Charge relay system (By similarity).
FT CARBOHYD 390 390 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 547 547 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 614 614 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 689 689 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 735 735 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 741 741 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 776 776 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 832 832 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 887 887 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1251 1251 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1385 1385 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1386 1386 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1454 1454 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1704 1704 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1743 AA; 194146 MW; 12DB363E2F729839 CRC64;

Query Match 23.3%; Score 523.5; DB 1; Length 1743;
Best Local Similarity 27.9%; Pred. No. 2.3e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

QY 19 LVGGQGVAVADTGLDTRG---NDS-----SMHEAPRGKITALVALGRNTNANDTNGH 68
Db 314 LRKGQQLSIADTGLDGSCHFFSDSKYPIPLSNVLNHR-KVVTYITSTSDSDSKVDGH 372

QY 69 GTHVAGSVLG-----NGSTNKGMAPQANLVFQSIMDSGGGLGGL--PSNLQTLFQSQAY 119
Db 373 GTHICGSAAGTPEDSSVNISSFSGLATDAKIAF---FDLASGSSSLTPPSDLKQLVQPLY 429

QY 120 SGARIHTNSGA-----AVNGAYITDSRVNDVYRKN-DMTILFAAGNEPGNGTIS--A 172
Db 430 DAGARVHCDSWGSVSVEGTGYSSTASIDDFLTHPDFFILRAAGN---NEQVLSLT 486

QY 173 PGTAKNAITVGATENLR-----PSFGSYADNI----- 199
Db 487 QSTAKNVIITGAHQTGHTHENYLTGPNYINQSSVDINQBELICDFDSRYCNYTTAQCCLES 546

QY 200 -----NHVAFSSRGPTKDGRIKPDVWAPGTFIL 228
Db 547 NATTGLASCCPTLLRKSVIDAANTOPLLNNENNICSFSSKGPHTDGRMKPALVAPGEYIT 606

QY 229 SARSSLA-----PDSSFWANHSKYAYMGSTMATPIVAGNVNAQREH-----F 272
Db 607 SARSGANTTDCGGDGL-PNTNALLA-ISGTSMATSPAAATLILRQLVLDGYPTGSI 664

QY 273 VNRGITPKPSLLKALIAAG-----ADIGLYPNGN-----QGWGRVT 311
Db 665 VESNKLPQPTGSLKALMINNAQLNGTFLQITSSSITPSNQVFENFAGASLVQGWGAIR 724

QY 312 LDKSLNVAVVNESS-----SLSTSOKATYSPT-- 338
Db 725 MSNWLHVNNNNNNNNNTSDGITPFGDGGDLRLVKPNQWKEESLSTGNTSYCTYK 784

QY 339 -----ATAGKPLK--ISLVSDAPASTTASVTLVNDLVL-----TAPNGT 378
Db 785 PSSSSNSGNNIPRVVATLVWTDPSYAGAKFNVLNNLDLTIYYRDNGSTIFYSNQGS 844

QY 379 QVGVNDFTSPYNDWGRNVFNAPQSGTYTIEVQAYNVVPGPQTF 429
Db 845 SFLG---LAPTQDT---LNNVEGIVHNPTPEMTYRFVWAGTNVPMGPQNF 889

RESULT 15
Q8T9W1_DICDI PRELIMINARY; PRT; 1825 AA.
AC Q8T9W1;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Serine protease/ABC transporter TagD (ABC transporter B family protein).
DE Name:tagD; ORFNames=DOB0191427;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_Taxid=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Anjard C., Loomis W.F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sucgang R., Barriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Roest R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny J., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchreiser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lousaged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodcock J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2003).
DR EMBL; AF466309; AAL74253.1; -; Genomic DNA.
DR EMBL; AAF01000133; EAL64354.1; -; Genomic DNA.
DR HSSP; P08716; 1MT0.
DR DictyBase; DDB0191427; tagD.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.

DR GO: GO:0016887; F:ATPase activity; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004289; F:subtilase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR003593; AAA ATPase.
DR InterPro: IPR011527; ABC_membrane_1.
DR InterPro: IPR001140; ABC_TM_transp.
DR InterPro: IPR003439; ABC_transp_like.
DR InterPro: IPR002029; Pept_S8_S53.
DR Pfam: PF00664; ABC_membrane; 1.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF00082; Peptidase_S8; 1.
DR PRINTS: PRO0723; SUBTILISIN.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS0929; ABC_TM1F; 1.
DR PROSITE: PS0211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS0893; ABC_TRANSPORTER_2; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; UNKNOWN_1.
DR PROSITE: PS00138; SUBTILASE_SER; UNKNOWN_1.
KW Protease.
SQ SEQUENCE 1825 AA; 202642 MW; E28160BC78613A3B CRC64;

Query Match 22.8%; Score 511.5; DB 2; Length 1825;
Best Local Similarity 27.9%; Pred. No. 1.5e-24;
Matches 164; Conservative 76; Mismatches 155; Indels 193; Gaps 22;

QY 19 LYGOQIVAVADTGLDTGR---NDS-----SMHEAFRGKITALYALGRNTNANDTNGH 68
DB 327 LRKGQQLSIADTGLDGHCFSDSDNNPIPNVSNLNRKVVYIGSL--HDNEDYVDGH 384

QY 69 GTHVAGSVLNG-----STNKGMAPQANLVFQSI-MDSGGGLGGLPSNLQTLFSQAYS 120
DB 385 GTHVCGSRAAGAPEDSSSLAISFSGLATDAKIAFFDLASDPNNPVPPEDEYSQLYQPLYN 444

QY 121 AGARIHTNSWA-----AVNGATTDSRNVDVVRKN-DWTILFAAGNEGPNGGTISAPGT 175
DB 445 AGARVHGDSWGSLSIQGYLGSYDDAGSIDFLYTHPDFIILRAAGNNEQYSSLLS-QAT 503

QY 176 AKNAITVGATENLRPSF----- 192
DB 504 AKNVITVGAETHSYTTDALEYSNFETVAKSTLNSLCQSPDDKVCYTTTAQCCTEYST 563

QY 193 -----GSYAD-----NINHVAQFSRGPTKDGRKPDVMAFGTIFLSA 230
DB 564 VKGLSGCCTSYIKNSYASIFSSQPELYNENNICSFSSKGPETHDGRKPDIVAPGQVITSA 623

QY 231 RSSLA-----PDSSFANHDSKYAYMGGTSMATPIVAGNVAQLREH----- 271
DB 624 RSGANTTTDQCGDSLPTNALLSE-----SGTSMATPLATAATTILRQYLVGYYPT 676

QY 272 --FVKNRGITTPKPSLLKALIAAGADIGLGP-----NGNGQWGRV 310
DB 677 GSIVESNKLQPTGSLKALMINNAQLLNGTFFLSSNTNTPSNVAVPTTFAGANFVQGWGSL 736

QY 311 TLDKSLNAVYVNESS-----SLSTSQKATYSFT----- 338
DB 737 RMSEWL---YVESGKPKPSRWVGIGELGDKKASNWKYSLSLTGQNVSYCYTYKPSSS 793

QY 339 --ATAGKP-LKISLWSDAPASTASVTLYNDLDLVITAPNGTQ----YVGNDFTSFYND 391
DB 794 GSNSSGIPRIVATLVMTDPPSYSGAKNLVNNLDLTMT---NTESEFIFYNSGGSSYNG 850

QY 392 N-----WGRNVENVF---INAPQSGTYTIEVQAYNVVPGPQTF 429
DB 851 TKGTTLPLQDSINNVEGIYTPINTKSEISFRPIAGTNIPIGPQNF 898